

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 8, 2005, 01:28:17 ; Search time 3431 Seconds  
(without alignments)  
6202.508 Million cell updates/sec

Title: US-10-663-157-3

Perfect score: 584

Sequence: 1 ggcgcgcgmngngcgaag.....agaattacctgtgtgtgcc 584

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_hic:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_gss1:\*

9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1          | 515.2 | 88.2        | 836    | 4  | BI465085    |
| 2          | 512   | 87.7        | 975    | 5  | BQ927810    |
| 3          | 498.6 | 85.4        | 882    | 5  | BQ688267    |
| 4          | 486   | 83.2        | 526    | 2  | BF433925    |
| 5          | 481.8 | 82.5        | 875    | 4  | BI544644    |
| 6          | 474.8 | 81.3        | 743    | 4  | BG773091    |
| 7          | 440.8 | 75.5        | 482    | 2  | BF512756    |
| 8          | 417.2 | 71.4        | 1118   | 2  | BE615766    |
| 9          | 413.6 | 70.8        | 452    | 7  | N49208      |
| 10         | 398   | 68.2        | 503    | 2  | BE049432    |
| 11         | 385   | 65.9        | 913    | 5  | BQ887029    |
| 12         | 385   | 65.9        | 3628   | 3  | AK043823    |
| 13         | 384.6 | 65.9        | 645    | 6  | CA333708    |
| 14         | 382.6 | 65.5        | 420    | 1  | AA918818    |
| 15         | 372   | 63.7        | 497    | 1  | AL138519    |
| 16         | 368.2 | 63.0        | 3597   | 3  | AK033529    |
| 17         | 366   | 62.7        | 824    | 2  | BE867582    |
| 18         | 364.6 | 62.4        | 600    | 6  | CA528743    |
| 19         | 355.6 | 60.9        | 829    | 4  | BI649863    |
| 20         | 349.8 | 59.9        | 732    | 1  | AI663485    |
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| 22         | 348.2 | 59.6        | 822    | 4  | BI649277    |
| 23         | 335.2 | 57.4        | 1039   | 7  | CF593305    |
| 24         | 323   | 55.3        | 521    | 2  | AW263837    |

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|----|-------|------|-----|---|----------|--------------------|
| 25 | 315.8 | 54.1 | 953 | 6 | CA976916 | CA976916 AGENCOURT |
| 26 | 306.8 | 52.5 | 766 | 4 | BG752486 | BG752486 602730981 |
| 27 | 291.8 | 50.0 | 528 | 1 | AU129537 | AU129537 AU129537  |
| 28 | 291.2 | 49.9 | 849 | 2 | BF687212 | BF687212 602102237 |
| 29 | 289.8 | 49.6 | 593 | 4 | BI544954 | BI544954 603242416 |
| 30 | 283   | 48.5 | 950 | 5 | BQ950513 | BQ950513 AGENCOURT |
| 31 | 279.8 | 47.9 | 486 | 7 | CN373267 | CN373267 170004241 |
| 32 | 279   | 47.8 | 759 | 4 | BI561782 | BI561782 603255204 |
| 33 | 270   | 46.2 | 912 | 2 | BF530378 | BF530378 602071685 |
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| 35 | 262.8 | 45.0 | 825 | 4 | BI110344 | BI110344 602900776 |
| 36 | 253   | 43.3 | 651 | 6 | BY731428 | BY731428 BY731428  |
| 37 | 238.4 | 40.8 | 637 | 2 | BB624973 | BB624973 BB624973  |
| 38 | 237.4 | 40.7 | 638 | 6 | BY718537 | BY718537 BY718537  |
| 39 | 223   | 38.2 | 744 | 5 | BU599647 | BU599647 AGENCOURT |
| 40 | 221.2 | 37.9 | 513 | 5 | BO555510 | BO555510 H4034803  |
| 41 | 218.8 | 37.5 | 678 | 9 | CG503364 | CG503364 OST50095  |
| 42 | 218.6 | 37.4 | 373 | 9 | CE182320 | CE182320 tigr-988  |
| 43 | 212   | 36.3 | 537 | 7 | CN298860 | CN298860 170004249 |
| 44 | 210.8 | 36.1 | 876 | 5 | BX389844 | BX389844 BX389844  |
| 45 | 208.8 | 35.8 | 405 | 7 | CN373259 | CN373259 170005319 |

#### ALIGNMENTS

RESULT 1

BI465085

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BI465085 836 bp mRNA linear EST 21-AUG-2001  
603206493F1 NIH\_MGC\_97 Homo sapiens cDNA clone IMAGE:5272054 5',  
mRNA sequence.  
BI465085  
BI465085.1 GI:15255741  
EST.  
Homo sapiens (human)  
Homo sapiens  
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC http://mgc.nhl.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs@mail.nih.gov  
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki  
Toshiyuki and Piero Carninci (RIKEN)  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM11686 row: j column: 23  
High quality sequence stop: 791.

FEATURES

source

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/clone="IMAGE:5272054"  
/lab\_host="DH10B"  
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/note="Organ: testis; Vector: pBluescriptR (modified  
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(gctcag); Oligo-dT primed using primer  
5'-TTTTTTTTTTTTTNN-3', size-selected for average  
insert size 2.2 kb and normalized to ROT 5. This is a  
primary library enriched for full-length clones and  
constructed using the Cap-trapper method (Carninci, in  
preparation). Library constructed by M. Brownstein  
(NIH/NHGRI, National Institutes of Health). Note: this is  
a NIH\_MGC Library."

ORIGIN

Query Match 88.2%; Score 515.2; DB 4; Length 836;  
Best Local Similarity 94.7%; Pred. No. 8.7e-116;  
Matches 551; Conservative 0; Mismatches 29; Indels 2; Gaps 2;

QY 1 GCGNCCGCGNNGNGCAAGTGTCTGAGCGCCCTTAGNGCCTCCCTTGGCGCTCCCTCC 60  
DB 189 GCGGCGCGCGCTGGCGAGTGTCTGAGCGCCCTTAGAGCTCTCTTGGCGCTCCCTCC 248  
QY 61 TCTGCCCGCGCTAGCAGTGTCAATGGGGTGTGGAGGTAGATGGGCTCCCGG-CCGGGA 119  
DB 249 TCTGCCCGCGCGCAGCAGTGTCAATGGGGTGTGGAGGTAGATGGGCTCCCGGCGCGGA 308  
QY 120 GCGGCGGTGGATGCGCGCTGGGAGAGCAGCCCGGATTCAGCTGCCCGCGCGCC 179  
DB 309 GCGGCGGTGGATGCGCGCTGGGAGAGCAGCCCGGATTCAGCTGCCCGCGCGCC 368  
QY 180 CC-GGGCACCTTCGAGTCTCCCGGTTCCAGCATCGGGGACCTCTCCGAGCAGCAGCACCGC 238  
DB 369 CCGGCGCGCCCTGGAGTCTCCCGGTTCCAGCATCGGGGACCTCTCCGAGCAGCAGCACCGC 428  
QY 239 CTTGCCCTCTGAGCGCGCATTCGCGCGCGAGCCAGCCAGCCACGATGATCGGGCTCCCT 298  
DB 429 CTTGCCCTCTGAGCGCGCATTCGCGCGCGAGCCAGCCAGCCACGATGATCGGGCTCCCT 488  
QY 299 TCTCCTGCTTGGATTCCTTAGCACCACACAGCTCAGCAGACAGAGGCTTCGAATCT 358  
DB 489 TCTCCTGCTTGGATTCCTTAGCACCACACAGCTCAGCAGACAGAGGCTTCGAATCT 548  
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DB 549 CATTTGGCACATACCGCCATGTTGACCGTGCACCGCGCGAGGTCTTAACCTGTGACAAAGTG 608  
QY 419 TCAGCAGGAACTATGTTCTGAGCATTTGTTACACAGCAAGCGTGGCGTCTGCAAGCAG 478  
DB 609 TCAGCAGGAACTATGTTCTGAGCATTTGTTACACAGCAAGCGTGGCGTCTGCAAGCAG 668  
QY 479 TTGCGCTGTGGGACCTTTACAGGAGATGAGATGGCATAGAGAAATGCCATGACGTAG 538  
DB 669 TGCCCTGTGGGACCTTTACAGGAGATGAGATGGCATAGAGAAATGCCATGACGTAG 728  
QY 539 TCAGCCATGCCCATGGCCATGATTGAGAAATTAACCTTTGTC 580  
DB 729 TCAGCAATGCCCATGGCCATGATCGAGAAATTAACCTTTGTC 770

RESULT 2  
BQ927810 975 bp mRNA linear EST 20-AUG-2002  
LOCUS AGENCOURT 882280 NIH\_MGC\_40 Homo sapiens cDNA clone IMAGE:6381568  
DEFINITION 5', mRNA sequence.

ACCESSION BQ927810  
VERSION BQ927810.1 GI:22342841  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 975)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-f@mail.nih.gov  
Tissue Procurement: DCTD/DTF  
cDNA Library Preparation: Rubin Laboratory  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLCM2571 row: p column: 17  
High quality sequence stop: 498.

## FEATURES

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/note="Organ: prostate; Vector: pOTB7; Site\_1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 87.7%; Score 512; DB 5; Length 975;  
Best Local Similarity 95.1%; Pred. No. 5.4e-115;  
Matches 557; Conservative 0; Mismatches 26; Indels 3; Gaps 3;

QY 1 GCGNCCGCGNNGNGCAAGTGTCTGAGCGCCCTTAGNGCCTCCCTTGGCGCTCCCTCC 60  
DB 151 GCGGCGCGCGCTGGCGAGTGTCTGAGCGCCCTTAGAGCTCTCTTGGCGCTCCCTCC 210  
QY 61 TCTGCCCGCGCTAGCAGTGTCAATGGGGTGTGGAGGTAGATGGGCTCCCGG-CCGGGA 119  
DB 211 TCTGCCCGCGCGCAGCAGTGTCAATGGGGTGTGGAGGTAGATGGGCTCCCGGCGCGGA 270  
QY 120 GCGGCGGTGGATGCGCGCTGGGAGAGCAGCGCGATTCAGCTGCCCGCGCGCGC 179  
DB 271 GCGGCGGTGGATGCGCGCTGGGAGAGCAGCGCGATTCAGCTGCCCGCGCGCGC 330  
QY 180 CC-GGGCACCTTCGAGTCTCCCGGTTCCAGCCATGGGGACCTCTCCGAGCAGCAGCACCGC 238  
DB 331 CCGGCGCGCCCTTCGAGTCTCCCGGTTCCAGCCATGGGGACCTCTCCGAGCAGCAGCACCGC 390  
QY 239 CTTGCCCTCTGAGCGCGCATTCGCGCGCGAGCCAGCCAGCAGATGATCGGGCTCCCT 298  
DB 391 CTTGCCCTCTGAGCGCGCATTCGCGCGCGAGCCAGCCAGCAGATGATCGGGCTCCCT 450  
QY 299 TCTCCTGCTTGGATTCCTTAGCACCACACAGCTCAGCCAGAAAGAGGCTTCGAATCT 358  
DB 451 TCTCCTGCTTGGATTCCTTAGCACCACACAGCTCAGCCAGAAAGAGGCTTCGAATCT 510  
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DB 511 CATTTGGCACATACCGCCATGTTGACCGTGCACCGCGCGAGGTCTTAACCTGTGCAAGTG 570  
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DB 571 TCAGCAGGAACTATGTTCTGAGCATTTGTTAACAACAGCGCTGGCGGTCTGAGCAG 629  
QY 479 TTGCGCTGTGGGACCTTTACAGGAGATGAGATGGCATAGAGAAATGCCATGACGTAG 538  
DB 630 TTGCGCTGTGGGACCTTTACAGGAGATGAGATGGCATAGAGAAATGCCATGACGTAG 689  
QY 539 TCAGCCATGCCCATGGCCATGATTGAGAAATTAACCTTTGTCGCC 584  
DB 690 TCAGCCATGCCCATGGCCATGATTGAGAAATTAACCTTTGTCGCCGCC 735

## RESULT 3

BQ688267 882 bp mRNA linear EST 15-JUL-2002  
LOCUS AGENCOURT 8047240 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6207591  
DEFINITION 5', mRNA sequence.

ACCESSION BQ688267  
VERSION BQ688267.1 GI:21813583  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 882)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LICM2363 row: 0 column: 16  
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Site\_2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCACGAG(G). Library constructed by  
Ling Hong in the laboratory of Gerald M. Rubin (University  
of California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 85.4%; Score 498.6; DB 5; Length 882;  
Best Local Similarity 98.9%; Pred. No. 1e-111;  
Matches 523; Conservative 0; Mismatches 4; Indels 2; Gaps 2;  
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Db 1 TCCTCTCCCGCGCGCAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCGCGCG 60  
Qy 117 GGAGCGCGCGTGTAGTCCGCGTGGCAGAGCAGCGCGGATTCAGCTGCCCGCGC 176  
Db 61 GGAGCGCGCGTGTAGTCCGCGTGGCAGAGCAGCGCGGATTCAGCTGCCCGCGC 120  
Qy 177 GCCCC-GCCCACTTGGAGTCCCGGTTTCAGCCATGGGACCTCTCCGAGCAGCAGCAC 235  
Db 121 GCCCGCGCGCGCTTGGAGTCCCGGTTTCAGCCATGGGACCTCTCCGAGCAGCAGCAC 180  
Qy 236 CGCCCTCGCTCTGAGCGCATGCGCCCGGAGCCACAGCCAGCATGATCGCGGCTC 295  
Db 181 CGCCCTCGCTCTGAGCGCATGCGCCCGGAGCCACAGCCAGCATGATCGCGGCTC 240  
Qy 296 CCTTCTCCTGCTGGATTCCTAGCACACAGCTCAGCCAGAACAGAGCGCTCGAA 355  
Db 241 CCTTCTCCTGCTGGATTCCTAGCACACAGCTCAGCCAGAACAGAGCGCTCGAA 300  
Qy 356 TCTCATTTGGCAGCATACCGCATGTTGACCGTCCACCGCGCAGGTCTAACCTGTGACAA 415  
Db 301 TCTCATTTGGCAGCATACCGCATGTTGACCGTCCACCGCGCAGGTCTAACCTGTGACAA 360  
Qy 416 GTGTCCAGCAGGAAACCTATGTCTGTAGCATTTGTACCAACAGCCTCGCGCTCTCAG 475  
Db 361 GTGTCCAGCAGGAAACCTATGTCTGTAGCATTTGTACCAACAGCCTCGCGCTCTCAG 420  
Qy 476 CAGTTGCCCTGTGGGGACCTTTACCAGGCATGAGATGGCATAGAGAAATGCCATGACTG 535  
Db 421 CAGTTGCCCTGTGGGGACCTTTACCAGGCATGAGATGGCATAGAGAAATGCCATGACTG 480

Qy 536 TACTCAGCCATGCCCATGCCAATGATGAGAAATACCTTGTGTGCTGCC 584  
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LOCUS 7q56g07.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3702349 3,  
DEFINITION similar to TR:O75505 O75509 TNFR-RELATED DEATH RECEPTOR-6,  
contains MER22.t2 PTR5 repetitive element ; mRNA sequence.  
ACCESSION BF433925  
VERSION 1 (bases 1 to 526)  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 526)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
DNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL, send email to:  
info@image.llnl.gov  
Seq primer: -40UP from Gibco  
High quality sequence stop: 427.  
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modified polylinker; Plasmid DNA from the normalized  
library NCI CGAP Lu5 was prepared, and as circles were  
made in vitro. Following HAP purification, this DNA was  
used as tracer in a subtractive hybridization reaction.  
The driver was PCR-amplified cDNAs from a pool of 5,000  
clones made from the same library (cloneIDs  
1414920-1417991 and 1520904-1522439). Subtraction by Bento  
Soares and M. Fatima Bonaudo."

Query Match 83.2%; Score 486; DB 2; Length 526;  
Best Local Similarity 97.7%; Pred. No. 1.2e-108;  
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Db 1 CCTCTCCTCTCTGCCCCGCGCAGCAGTGCACATGGGGTGTGGAGTAGATGGGCTCCC 60  
Qy 112 GG-CCGGAGCGCGCGTGTAGTCCGGCTGGGCAGNAGCAGCGCGATTCAGCTGCC 170  
Db 61 GGCCCGGAGCGCGCGTGTAGTCCGGCTGGGCAGNAGCAGCGCGATTCAGCTGCC 120  
Qy 171 CCGCGCGCCCC-GGCCACCTTGGAGTCCCGGTTTTCAGCCATGGGGACCTCTCCGAGCAG 229  
Db 121 CCGCGCGCCCCGGCGCCCTTCGAGTCCCGGTTTTCAGCCATGGGGACCTCTCCGAGCAG 180  
Qy 230 CAGCACCGCCCTTCGCTCTTCGAGCGCATCGCCCGCGCAGCCACGACCGATGATCGC 289

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Db 181 CAGCACGGCCCTCGCTCTGACGGCGCATGCGCCCGCGAGCCACAGCCACGATGATCG 240
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Db 241 GGGCTCCCTTCCTCTGATTCCTAGCAGCCACACAGCTCAGCCAGACAGAGCG 300
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Db 301 CTCGAATCTCATTTGGCACATACCGCCATGTTGACCGTGCACCGGCGAGTGCTAACCTG 360
QY 410 TGCAAGTGTCCAGCAGGAACCTATGCTCTGAGCATTTGACAAACAGGCTGCGCT 469
Db 361 TGCAAGTGTCCAGCAGGAACCTATGCTCTGAGCATTTGACAAACAGGCTGCGCT 420
QY 470 CTCGACAGTGGCCCTGTGGGACCTTTACCGGCGATGAGATGGCATGAGAAATGCCA 529
Db 421 CTCGACAGTGGCCCTGTGGGACCTTTACCGGCGATGAGATGGCATGAGAAATGCCA 480
QY 530 TGAATCTAGTACGACCATGCCATGGCCATGATTGAGAAATTAACCT 575
Db 481 TGAATCTAGTACGACCATGCCATGGCCATGATTGAGAAATTAACCT 526

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RESULT 5
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DEFINITION mRNA sequence.
ACCESSION BI544644
VERSION BI544644.1 GI:15431956
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11719 row: h column: 24
High quality sequence stop: 785.
FEATURES
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pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
(GTCGAG); Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.5 kb and normalized to 10^5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes of Health). Note: this
is a NIH_MGC Library."

```

ORIGIN

Query Match

82.5%; Score 481.8; DB 4; Length 875;

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Best Local Similarity 95.1%; Pred. No. 1.4e-107;
Matches 558; Conservative 0; Mismatches 23; Indels 6; Gaps 6;
QY 1 GGGCCGCGGNGNGCAGAGTGTGAGCGCCCTAGNGCCTCTCCCTGCGGCTCCCTCC 60
Db 220 GCGGCGCGGCGCTGGGCGAGGTGTGAGCGCCCTAGAGCCTCTCCCTGCGGCTCCCTCC 279
QY 61 TCTGCGCGCGCTAGCAGTGCACATGGGCTGTGTGAGGTAGATGGCTCCCGG-CGGGA 119
Db 280 TCTGCGCGCGCGCAGCAGTGCACATGGGCTGTGTGAGGTAGATGGCTCCCGGCGGGA 339
QY 120 GCGCGCGTGTGATGCGGCGCTGGGCGAGCAGCGCCGATTTCCAGCTGCCCCGCGCGC 179
Db 340 GCGCGCGTGTGATGCGGCGCTGGGCGAGCAGCGCGGATTTCCAGCTGCCCCGCGCGC 399
QY 180 CC-GGCGACCTTGCAGTCCCGGTTTCCAGCCTAGGCGACCTCTCGAGCAGCAGCACCGC 238
Db 400 CCGGCGCGCGCTGCGAGTCCCGGTTTCCAGCCTAGGCGACCTCTCGAGCAGCAGCACCGC 459
QY 239 CCTCGCCTCTCGAGCGCATCGCCGCGGAGCCACAGCAGATGATCGCGGCTCCCT 298
Db 460 CTTGCGCTCTCGAGCGCATCGCCGCGGAGCCACAGCAGATGATCGCGGCTCCCT 519
QY 299 TCTCTGCTTGGATTCCTTAGCACACACAGCTCAGCCAGAACAGAA-GGCTCGAATC 357
Db 520 TCTCTGCTTGGATTCCTTAGCACACACAGCTCAGCCAGAACAGAAAGGGCTCGAATC 579
QY 358 TCATTTGGCAC-ATACCGCATGTTACCGTCCCGGCGGAGGCTTAACCTGTGCAAG 416
Db 580 TCATTTGGCACAAATACCGCATGTTACCGTCCCGGCGGAGGCTTAACCTGTGCAAG 639
QY 417 TGTCCAGCAGGAACCTATGCTCTGAGCATTTGACAAACAGCCTGCGCTCTGCAG- 475
Db 640 TGTCCAGCAGGAACCTATGCTCTGAGCATTTGACAAACAGCCTGCGCTCTGCAGC 699
QY 476 CAGTTGCCCTGTGGGAGCTTTTACAGGATGAGAAATGSCATAGAGAAATGCCATG-ACT 534
Db 700 CAGTTGCCCTGTGGGAGCTTTTACAGGATGAGAAATGSCATAGAGAAATGCCATG- 759
QY 535 GTAGTCAGCCATGCCCATGGCAATGATTGAGAAATTAACCTTGCT 581
Db 760 GTAGTCAGCCATGGCAATGATTGAGAAATTAACCTTGCT 806

RESULT 6
BI544644
LOCUS 602721804F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4838808 5',
DEFINITION mRNA sequence.
ACCESSION BG773091
VERSION BG773091.1 GI:14083744
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10773 row: g column: 01
High quality sequence stop: 736.
FEATURES
Location/Qualifiers

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source 1. 743
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4838808"
/lab_host="DH10B"
/clone_lib="NIH_MGC_97"
/notes="Organ: testis; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
(gtcgag); Oligo-dT primed using primer
5'-TTTTTTTTTTTTTNN-3', size-selected for average
insert size 2.2 kb and normalized to 10^5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes of Health). Note: this is
a NIH_MGC Library."

ORIGIN
Query Match 81.3%; Score 474.8; DB 4; Length 743;
Best Local Similarity 97.1%; Pred. No. 7.1e-106;
Matches 501; Conservative 0; Mismatches 13; Indels 2; Gaps 2;

QY 1 GCGNCCGCGGNGNGCAAGGTGCTGAGCGCCCTAGNGCCTCCTTGCCTCCCTCCCTCC 60
DB 228 GCGGCGCGCGCGCTGGCGCAGGTGCTGAGCGCCCTAGAGCCTCCTTGGCGCTCCCTCC 287
QY 61 TCTGCCCGCGGTAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCGG-CCGGGA 119
DB 288 TCTGCCCGCGCGCAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCGCGCGGGA 347
QY 120 GCGCGCGGTGGATGCGCGCTGGGCGAGAGCAGCGCCGATTCAGCTGCCCGCGCGCC 179
DB 348 GCGCGCGGTGGATGCGCGCTGGGCGAGAGCAGCGCCGATTCAGCTGCCCGCGCGCC 407
QY 180 CC-GGCCACTTGTGGAGTCCCGGTTGAGCATTGGGAGCTCTCCGAGCAGCAGCCGC 238
DB 408 CCGGCGCGCGCTGCGATGCTCCCGGTTGAGCATTGGGAGCTCTCCGAGCAGCAGCCGC 467
QY 239 CTTGCTCTCTGAGCGCGATCGCGCGCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 298
DB 468 CTTGCTCTCTGAGCGCGATCGCGCGCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 527
QY 299 TCTCTGCTTGGATTCTTACGACACACAGCTCAGCCAGCAGCAGCAGCAGCAGCAGCAG 358
DB 528 TCTCTGCTTGGATTCTTACGACACACAGCTCAGCCAGCAGCAGCAGCAGCAGCAGCAG 587
QY 359 CATTTGCACATACCGCATGTTGACCGTGCACCGCGCAGGTGCTAACCTGTGACAAAGTG 418
DB 588 CATTTGCACATACCGCATGTTGACCGTGCACCGCGCAGGTGCTAACCTGTGACAAAGTG 647
QY 419 TCCAGCAGGAACCTATGCTCTGAGCATTCATACCAAGCAGCAGCAGCAGCAGCAGCAG 478
DB 648 TCCAGCAGGAACCTATGCTCTGAGCATTCATACCAAGCAGCAGCAGCAGCAGCAGCAG 707
QY 479 TTGCGCTGTGGGACCTTTTACCGGATGAGATGG 514
DB 708 TTGCGCTGTGGGACCTTTTACCGGATGAGATGG 743

RESULT 7
BF512756
LOCUS BF512756
DEFINITION UI-H-BMI-amm-f-03-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone
IMAGE:3070588 3', mRNA sequence.
ACCESSION BF512756
VERSION BF512756.1
KEYWORDS G1:11597935
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 482)
```

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapsb@mail.nih.gov](mailto:cgapsb@mail.nih.gov)  
Oligo-dT track not found, Not 1 site shown in beginning of sequence  
is likely internal to the message. cDNA library preparation: M.B.  
Soares Lab Clone distribution: NCI-CGAP clone distribution  
Information can be found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html) The following repetitive  
elements were found in this cDNA sequence: 188-190,  
>GC rich#Low complexity  
Seq primer: M13 Forward  
POLYA=No.

Location/Qualifiers  
1. 482  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3070588"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NCI\_CGAP\_Sub7"  
/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; NCI CGAP Sub7  
is a subtracted library derived from NCI CGAP Sub6. The  
NCI CGAP Sub7 library had 12 million recombinants. A  
single-stranded DNA preparation of NCI CGAP Sub6 was used  
as a tracer in a subtractive hybridization with a driver  
comprising: the IMAGE pool (NCI CGAP Kid3 pool 1 LLAM  
3334-3337, 3682-3683, 3798-3803 (IMAGE CloneIDs  
1322376-1323911, 1456008-1456775, 1500552-1502855);  
NCI CGAP Kid5 pool 1 LLAM 3338-3342, 3722-3725, 3776-3778  
(IMAGE CloneIDs 1323912-1325831, 1471368-1472803,  
1492104-1493255); NCI CGAP Lys pool 1 LLAM 3575-3582,  
3851-3854 (IMAGE CloneIDs 1414920-1417991,  
1520904-1522439); NCI CGAP GC4 pool 1 LLAM 3164-3167,  
3716-3720, 3733-3735 (IMAGE CloneIDs  
1257096-1258631, 1469064-1470983, 1475592-1476743);  
NCI CGAP Pr22 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068  
(IMAGE CloneIDs 985608-986759, 1101192-1101959,  
1217928-1220615); NCI CGAP Col0 pool 1 LLAM 2644-2653,  
2871-2872 (IMAGE CloneIDs  
1057416-1061255, 1144584-1145351). (6% of the driver  
population), plus a pool of 3,840 arrayed clones from  
NCI CGAP Sub1 (IMAGE CloneIDs 2708616-2710535) and  
NCI CGAP Sub2 (IMAGE CloneIDs 2710536-2712455) (4% of  
the driver population), plus a pool of 11,136 clones from  
NCI CGAP Sub3 (IMAGE CloneIDs 2712456-2723591) (10% of  
the driver population), plus a pool of 5,472 clones from  
NCI CGAP Sub4 (IMAGE CloneIDs 2723592-2729326) (40% of the  
driver population), plus a pool of 4032 clones from  
NCI CGAP Sub6 (IMAGE CloneIDs 2728969-2733190) (40% of the  
driver population). Subtraction was performed as  
previously described (Bonaldi, Lennon & Soares (1996):  
Normalization and Subtraction: Two Approaches To  
Facilitate Gene Discovery. Genome Research 6, 791-806.  
TAG\_SEQ=None found"

Query Match 75.5%; Score 440.8; DB 2; Length 482;  
Best Local Similarity 96.9%; Pred. No. 1.5e-97;  
Matches 467; Conservative 0; Mismatches 13; Indels 2; Gaps 2;  
QY 2 CGNCCGCGGNGNGCAAGGTGCTGAGCGCCCTAGNGCCTCCTTGCCTCCCTCCCTCC 61  
DB 1 CGGCGCGCGCGCTGGCGCAGGTGCTGAGCGCCCTAGAGCCTCCTTGGCGCTCCCTCC 60  
QY 62 CTGCCCCGCGGTAGCAGTGCACATGGGGTGTGGAGGTAGATGGCTCCCGG-CCGGGAG 120  
DB 61 CTGCCCCGCGGACGAGTGCACATGGGGTGTGGAGGTAGATGGGTCCCGGCGCGGAG 120  
QY 121 GCGGCGGTGGATGCGCGCGCTGGGCGAGCAGCGCGGATTCAGCTGCCCGCGCGCCC 180

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Db      121 GCGGCGGTGGATGCGCGCTGGGAGAGCAGCCGCCGATTCAGCTGCCCGCGCGCC 180
Qy      181 C-GGCCACCTTGGAGTCCCGGTTCAGCCATGGGACCTCCGAGAGCAGCAGCCGC 239
Db      181 CGGCGCCCTCGGAGTCCCGGTTCAGCCATGGGACCTCCGAGAGCAGCAGCCGC 240
Qy      240 CTCGCTCTCTGAGCGCGCATCGCCCGGAGCCACAGCCACAGATGATCGCGGCTCCCTT 299
Db      241 CTCGCTCTCTGAGCGCGCATCGCCCGGAGCCACAGCCACAGATGATCGCGGCTCCCTT 300
Qy      300 CTCGCTCTCTGAGTTCCTTAGCACCCACAGCTCAGCCAGAAAGAGCCCTCGAATCTC 359
Db      301 CTCGCTCTCTGAGTTCCTTAGCACCCACAGCTCAGCCAGAAAGAGCCCTCGAATCTC 360
Qy      360 ATTGGACATACCGCCATGTTGACCGTGCACCGCCAGGTCGTAACTGTGACAGTGT 419
Db      361 ATTGGACATACCGCCATGTTGACCGTGCACCGCCAGGTCGTAACTGTGACAGTGT 420
Qy      420 CCAGCAGGAACCTATGCTCTGAGCATTTGACCAACAGCTGCGCGTCTGCAGCAGT 479
Db      421 CCAGCAGGAACCTATGCTCTGAGCATTTGACCAACAGCTGCGCGTCTGCAGCAGT 480
Qy      480 TG 481
Db      481 TG 482
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RESULT 8
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LOCUS    601279916F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622107 5',
DEFINITION
mRNA sequence.
ACCESSION BE615766
VERSION    BE615766.1 GI:9897365
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE      NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL    National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT    Unpublished (1999)
           Contact: Robert Strauberg, Ph.D.
           Email: csapbs-@email.nih.gov
           Tissue Procurement: ATCC
           CDNA Library Preparation: Ling Hong/Rubin Laboratory
           CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLCM296 row: o column: 04
           High quality sequence stop: 716.
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FEATURES
source    Location/Qualifiers
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            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:3622107"
            /tissue_type="adenocarcinoma"
            /lab_host="DH10B (phage-resistant)"
            /clone_lib="NIH_MGC_39"
            /note="Organ: pancreas; Vector: pOTB7; Site1: XhoI;
            Site 2: EcoRI; cDNA made by oligo-dT priming.
            Directionally cloned into EcoRI/XhoI sites using the
            following 5' adaptor: GGCACGAG(G). Library constructed
            by Ling Hong in the laboratory of Gerald M. Rubin
            (University of California, Berkeley) using ZAP-cDNA
            synthesis kit (Stratagene) and Superscript II RT (Life
            Technologies)."
```

ORIGIN

```
Query Match      71.4%; Score 417.2; DB 2; Length 1118;
Best Local Similarity 98.7%; Pred. No. 1e-91;
Matches 452; Conservative 0; Mismatches 3; Indels 3; Gaps 3;
Qy      130 GATCGGCGCTGGGAGAGCAGCCGATTCAGCTGCCCGCGCGCCCGCC 188
Db      1 GATCGGCGCTGGGAGAGCAGCCGATTCAGCTGCCCGCGCGCGCGCCCGCC 60
Qy      189 TTGCGAGTCCCGGTTCAGCCATGGGACCTTCGAGCAGCAGCAGCCCTCCCTCC 248
Db      61 CTCGAGTCCCGGTTCAGCCATGGGACCTTCGAGCAGCAGCAGCCCTCCCTCC 120
Qy      249 TGCAGCCGATCGCCCGCGGACACAGCAGATGATCGCGGGCTCCCTTCTCTGCTT 308
Db      121 TGCAGCCGATCGCCCGCGGAGCCACAGCCAGATGATCGCGGGCTCCCTTCTCTGCTT 180
Qy      309 GGATTCCTTAGCACCCACAGCTCAGCCAGAAAGAGGCTCGAATCTCAATGGCACA 368
Db      181 GGATTCCTTAGCACCCACAGCTCAGCCAGAAAGAGGCTCGAATCTCAATGGCACA 240
Qy      369 TACCGCCATGTTGACCGTGCACCGCCAGGTCCTAACTGTGACAAAGTGTCCACAGA 428
Db      241 TACCGCCATGTTGACCGTGCACCGCCAGGTCCTAACTGTGACAAAGTGTCCACAGA 300
Qy      429 ACCTATGCTCTGAGCATTTGACCAACAGCCCTGCGCTCTGCAGCAGTGGCCCTGTG 488
Db      301 ACCTATGCTCTGAGCATTTGACCAACAGCCCTGCGCTCTGCAGCAGTGGCCCTGTG 360
Qy      489 GGGACCTTTACAGCAGCTGA-GAATGGCATAGAG-AAATGGCATGACTGTAGTCAGCCAT 546
Db      361 GGGACCTTTACAGCAGCTGA-GAATGGCATAGAG-AAATGGCATGACTGTAGTCAGCCAT 420
Qy      547 GCCCATGCCCATGATTGAGAAATTTACCTTGTGCTGCC 584
Db      421 GCCCATGCCCATGATTGAGAAATTTACCTTGTGCTGCC 458
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RESULT 9
N49208
LOCUS    N49208
DEFINITION
y48e08.s1 Soares multiple sclerosis 2NDHMSF Homo sapiens cDNA
clone IMAGE:280262 3', mRNA sequence.
ACCESSION N49208
VERSION    N49208.1 GI:1190374
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
           1 (bases 1 to 452)
           Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
           Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
           Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
           Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
           Wilson,R.
           The WashU-Merck EST Project
           Unpublished (1995)
           Contact: Wilson RK
           Washington University School of Medicine
           4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
           Tel: 314 286 1800
           Fax: 314 286 1810
           Email: est@watson.wustl.edu
           This clone is available royalty-free through LLNL; contact the
           IMAGE Consortium (info@image.llnl.gov) for further information.
           Possible reversed clone: polyT not found
           Seq primer: m13 -40 forward
           High quality sequence stop: 390.
FEATURES
source    Location/Qualifiers
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            /mol_type="mRNA"
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/db\_xref="GDB:3898638"  
/db\_xref="taxon:9606"  
/clone="IMAGE:280262"  
/sex="male"  
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/dev\_stage="Age 46"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares multiple sclerosis 2NbHMSp"  
/note="Vector: p773D (Pharmacia) with a modified  
polylinker V type; phagemid; Site 1: Not I; Site 2: Eco  
RI; 1st strand cDNA was primed with a Not I - oligo(dT)  
primer [5'  
TGTTACCAATCTGAAGTGGGCGCGCATTTTTTTTTTTTTTTT 3']  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified p773 vector  
(Pharmacia). Library went through one round of  
normalization to a Cot = 5. Library constructed by Bento  
Soares and M.Fatima Bonaldo. RNA from 4 multiple sclerosis  
lesions from one patient was kindly provided by Dr. Kevin  
G. Becker (NINDS/NIH). "

## ORIGIN

Query Match 70.8%; Score 413.6; DB 7; Length 452;  
Best Local Similarity 98.5%; Pred. No. 7.1e-91;  
Matches 445; Conservative 0; Mismatches 4; Indels 3; Gaps 2;  
QY 1 GCGNCCGNGNGNGCAAGTGCTGAGCGCCCTAGNGCCTCCCTTGGCGGCTCCCTCC 60  
DB 1 GCGNCCGNGNGNGCAAGTGCTGAGCGCCCTAGNGCCTCCCTTGGCGGCTCCCTCC 60  
QY 61 TCTGCCCGCGGTAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCGCGGGAG 120  
DB 61 TCTGCCCGCGGTAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCGCGGGAG 120  
QY 121 CGGCGGTGATGCGGCGCTGGGAGAGCAGCGCGCGGATTCAGCTGCGCGCGGCC 180  
DB 121 CGGCGGTGATGCGGCGCTGGGAGAGCAGCGCGCGGATTCAGCTGCGCGCGGCC 180  
QY 181 CGGCGCTTGGCGAGTCCCGGTTCAGCGATGGGACCTCTCCGAGCAGCAGCGGCC 240  
DB 181 CGGCGCTTGGCGAGTCCCGGTTCAGCGATGGGACCTCTCCGAGCAGCAGCGGCC 240  
QY 241 TCGCCTCTGAGCGGATCCCGCGGAGCCAGCAGCAGATGATCGCGGCTCCCTTC 300  
DB 241 TCGCCTCTGAGCGGATCCCGCGGAGCCAGCAGCAGATGATCGCGGCTCCCTTC 300  
QY 301 TCTGTGTTGATTCCTTAGCACCACAGCTCAGCCAGAACAGAGGCTCGAATCTCA 360  
DB 301 TCTGTGTTGATTCCTTAGCACCACAGCTCAGCCAGAACAGAGGCTCGAATCTCA 360  
QY 361 TT-GGCACATACCGCATGTGACCGTGCCACCGCGGAGTGTAACT--GTGACAAGT 417  
DB 361 TTGGGCACATACCGCATGTGACCGTGCCACCGCGGAGTGTAACTTTGTGACAAGT 420  
QY 418 GTCCAGCAGGAACCTATGTCTCTGAGCATGT 449  
DB 421 GTCCAGCAGGAACCTATGTCTCTGAGCATGT 452

RESULT 10  
BE049432

LOCUS BE049432 503 bp mRNA linear EST 08-JUN-2000  
DEFINITION x86d09.x1 NCI CGAP Pan1 Homo sapiens cDNA clone IMAGE:2834897 3'  
similar to TR:O75509 O75509 TNFR-RELATED DEATH RECEPTOR-6.  
; contains PTR5.t2 PTR5 PTR5 repetitive element ; mRNA sequence.

ACCESSION  
BE049432

VERSION BE049432.1 GI:8366487

## KEYWORDS

SOURCE EST.

## ORGANISM

Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 503)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: rgs@nih.gov  
Life Technologies catalog #: 11548-013  
DNA sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LINL, send email to:  
info@image.lnl.gov

Possible reversed clone: similarity on wrong strand  
Seq primer: -40UP from Gibco  
High quality sequence stop: 438.

FEATURES  
source

1..503  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2834897"  
/tissue\_type="adenocarcinoma"  
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/clone\_lib="NCI CGAP Pan1"  
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: SalI;  
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.72 kb. Life Technologies catalog #: 11548-013"

## ORIGIN

Query Match 68.2%; Score 398; DB 2; Length 503;  
Best Local Similarity 90.8%; Pred. No. 4.9e-87;  
Matches 455; Conservative 0; Mismatches 40; Indels 6; Gaps 3;  
QY 19 AGTGCTGAGCGCCCTAGNGCCTCCCTTGGCGGCTCCCTCTCTGCGCGCGGTAGCAG 78  
DB 6 AGTGCTGAGCGCCCTAGNGCCTCCCTTGGCGGCTCCCTCTCTGCGCGCGGTAGCAG 61  
QY 79 TGCACATGGGGTGTGGAGGTAGATGGGTCTCCGCGGAGCGCGGTGATGCGGC 137  
DB 62 TGCACATGGGGTGTGGAGGTAGATGGGTCTCCGCGGAGCGCGGTGATGCGGC 121  
QY 138 GCTGGGCGAGAGCAGCGCGGATTCAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 196  
DB 122 GCTGGGCGAGAGCAGCGCGGATTCAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 181  
QY 197 CCGCGGTTAGCCATGGGACCTCTCGAGCAGCAGCAGCGCGCTCGCCTCTGCGAGCG 256  
DB 182 CCGCGGTTAGCCATGGGACCTCTCGAGCAGCAGCAGCGCGCTCGCCTCTGCGAGCG 241  
QY 257 CATCGCGCGGAGCAGCAGCAGATGATCGCGGCTCCCTCTCTGCTTGGATTCT 316  
DB 242 CATCGCGCGGAGCAGCAGCAGATGATGCGGGCTCCCTCTCTGCTTGGATTCT 301  
QY 317 TAGCACCACACAGCTCAGCCAGAACAGAGGCTCGAATCTCATTTGGCACATACCGCA 376  
DB 302 TAGCACCACACAGCTCAGCCAGAACAGAGGCTCGAATCTCATTTGGCACATACCGCA 361  
QY 377 TGTTCACGTCACCGCGGAGGTGCTTAACCTGTGACAAAGTGTCCAGCAGAACCTATGT 436  
DB 362 TGTTCACGTCACCGCGGAGGTGCTTAACCTGTGACAAAGTGTCCAGCAGAACCTATGT 421  
QY 437 CTCTGAGCATTTGACCAACACAGAGCTGCGCGCTCTGAGCATGTTGCCCTGTGGGACCTT 496  
DB 422 CTCTGAGCATTTGAGCAACCAAGCTGCGCGCTCTGAGCATGTTGCCCTGTGGGACCTT 481  
QY 497 TACCAGGCATGAGAAATGGCAT 517  
DB 482 TACCAGGCATGAGAAATGGCAT 502

RESULT 11  
BQ887029

**LOCUS**  
**DEFINITION** BQ887029 913 bp mRNA linear EST 16-AUG-2002  
 AGENCOURT 8752338 NIH\_MGC\_130 Mus musculus cDNA clone IMAGE:6333538  
 5' mRNA sequence.  
**ACCESSION** BQ887029  
**VERSION** BQ887029.1 GI:22279043  
**KEYWORDS** EST.  
**SOURCE** Mus musculus (house mouse)  
**ORGANISM**  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
**REFERENCE**  
**AUTHORS** NIH-MGC <http://mgc.nci.nih.gov/>.  
**TITLE** National Institutes of Health, Mammalian Gene Collection (MGC)  
**JOURNAL** Unpublished (1999)  
**COMMENT** Contact: Robert Strausberg, Ph.D.  
 Email: [gsapbs-remail.nih.gov](mailto:gsapbs-remail.nih.gov)  
 Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freeman,  
 Ph.D.  
 cDNA Library Preparation: ResGen, Invitrogen Corp  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLAM1792 row: 0 column: 11  
 High quality sequence stop: 735.

# **FEATURES**

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# **ORIGIN**

**Query Match** 65.9%; Score 385; DB 5; Length 913;  
**Best Local Similarity** 82.0%; Pred. No. 8.2e-84;  
**Matches** 493; Conservative 0; Mismatches 91; Indels 17; Gaps 4;

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 DB 401 GTGGGCGGAGCGCGCGCGCGCGCTGCGAGCGCGCGAGCTCGGCATGGGACCGGGC 460  
 QY 224 GAGCAGCAGCAGCGCGCTCGCTCTGTCAGCGCGCATCGCCCGCGAGCAGCAGCAGAT 283  
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 QY 464 GCGGCTCTGACAGTGTGCGGCTGCGGACCTTTACGAGGATGAGATGGATGAGAGNA 523  
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**RESULT** 12  
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 insert sequence.  
**ACCESSION** AK043823  
**VERSION** AK043823.1 GI:26335926  
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**SOURCE** Mus musculus (house mouse)  
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
**REFERENCE**  
 1 Carninci,P. and Hayashizaki,Y.  
**TITLE** High-efficiency full-length cDNA cloning  
**JOURNAL** Meth. Enzymol. 303, 19-44 (1999)  
**MEDLINE** 99279253  
**PUBMED** 10349636  
**REFERENCE**  
 2 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,  
 Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
**TITLE** Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes  
**JOURNAL** Genome Res. 10 (10), 1617-1630 (2000)  
**MEDLINE** 20499374  
**PUBMED** 11042159  
**REFERENCE**  
 3 Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,  
 Konno,H., Akiyama,J., Nishi,K., Kitsuunai,T., Tashiro,H., Itoh,M.,  
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 Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J.,  
 Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.  
**TITLE** RIKEN integrated sequence analysis (RISA) system-384-format  
 sequencing pipeline with 384 multicapillary sequencer  
**JOURNAL** Genome Res. 10 (11), 1757-1771 (2000)  
**MEDLINE** 20530913  
**PUBMED** 11076861  
**REFERENCE**  
 4 The RIKEN Genome Exploration Research Group Phase II Team and the  
 PANTOM Consortium.  
**TITLE** Functional annotation of a full-length mouse cDNA collection  
**JOURNAL** Nature 409, 685-690 (2001)  
**REFERENCE**  
 5 The FANTOM Consortium and the RIKEN Genome Exploration Research  
 Group Phase I & II Team.  
**TITLE** Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs  
**JOURNAL** Nature 420, 563-573 (2002)  
**REFERENCE**  
 6 (bases 1 to 3628)  
 Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,  
 Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,  
 Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,  
 Horii,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,  
 Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,W.,

Koya.S., Kurihara,C., Mateuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saito,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

**TITLE**  
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

**COMMENT**  
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL:http://genome.gsc.riken.jp/  
URL:http://fantom.gsc.riken.jp/.

# FEATURES

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Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
1 (bases 1 to 645)  
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapsb@mail.nih.gov  
cDNA Library Preparation:  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL  
DNA Sequencing by: National Institutes of Health Intramural  
Sequencing Center (NISC)  
Clone distribution: NCI-CCAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
infoimage.llnl.gov  
Plate: L1AM12387 row: C column: 23  
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/dev\_stage="adult, 11 week"

# ORIGIN

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Best Local Similarity 82.0%; Pred. No. 9.9e-84;  
Matches 493; Conservative 0; Mismatches 91; Indels 17; Gaps 4;  
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Db |||||  
QY 60 CTC-----TGCCGCGCGGTAGCAGTCACATGGGGTGTGGAGGTAGATGGGCTC-C 110  
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QY 819 C 819  
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# FEATURES

## source

CA333708  
LOCUS  
DEFINITION  
IMAGE:5599054.5', mRNA sequence.  
CA333708.1 GI:24551806  
EST.  
Rattus norvegicus (Norway rat)  
Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
1 (bases 1 to 645)  
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapsb@mail.nih.gov  
cDNA Library Preparation:  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL  
DNA Sequencing by: National Institutes of Health Intramural  
Sequencing Center (NISC)  
Clone distribution: NCI-CCAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
infoimage.llnl.gov  
Plate: L1AM12387 row: C column: 23  
Seq primer: M13RPI reverse primer (ABI).  
Location/Qualifiers  
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/dev\_stage="adult, 11 week"

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post-castration, average insert size 2.7 kb),  
NCI CGAP Pr29 (dorsolateral prostate from 11 wk male, 5  
days post-castration, average insert size 2.2 kb) and  
NCI CGAP Pr42 (dorsolateral prostate from 11 wk male, 7  
days post-castration, average insert size 2.2 kb).  
Constructed by Life Technologies/Invitrogen. Note: this is  
a NCI CGAP Library."

## ORIGIN

Query Match 65.9%; Score 384.6; DB 6; Length 645;  
Best Local Similarity 82.0%; Pred. No. 9.8e-84;  
Matches 493; Conservative 0; Mismatches 90; Indels 18; Gaps 4;  
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SOURCE Homo sapiens (human)

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## Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 420)

## AUTHORS

NCI CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

## TITLES

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

## JOURNAL

Unpublished (1997)

## COMMENT

Contact: Robert Strausberg, Ph.D.

Email: [cgapsb-r@mail.nih.gov](mailto:cgapsb-r@mail.nih.gov)

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Sequencing by: Greg Lennon, Ph.D.

Clone Distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

[www.bio.llnl.gov/bbrp/image/image.html](http://www.bio.llnl.gov/bbrp/image/image.html)

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double-stranded cDNA was ligated to Eco RI adaptors,

(Pharmacia), digested with Not I and cloned into the Not

I and Eco RI sites of the modified pT7T3 vector. mRNA

source: 2 pooled kidneys. Library went through one round

of normalization. Library constructed by Bento Soares and

M. Fatima Bonaldo."

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Best Local Similarity 97.2%; Pred. No. 2.9e-83;

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QY 210 ATGGGGACCTCTCCGAGCAGCAGCAGCGCGCTCGCTCTCGCGCGCGCGCGCGCG 269

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QY 330 GGTACGCCAGACAGAGGCGCTCGAATCTCATTTGGCAGATATCGGCCATGTTGACCGTGC 389

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ACCESSION  AL138519
VERSION    AL138519.1 GI:6862557
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SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 497)
AUTHORS   Ansoerge,W., Wirkner,U., Mewes,W., Weil,B. and Wiemann,S.
TITLE     EST (Ansoerge,W., Wirkner,U., Mewes,H.W., Weil,B. and Wiemann,S.)
JOURNAL   Unpublished (1999)
COMMENT    Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by EMBL (European Molecular Biology Laboratories,
            Heidelberg/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            No sl sequence available.
            This clone (DKFZp761B2115) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES   Location/Qualifiers
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## RESULT 15

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AL138519
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

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Matches 443; Conservative 0; Mismatches 20; Indels 9; Gaps 5;

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Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY  133 CGGCGCTGGGAGACAGCGCGGATTCAGCTGCCCGCGCGCCCG-GGCCACCTTG 191
Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY  61  CGGCGCTGGGAGACAGCGCGGATTCAGCTGCCCGCGCGCCCGCGCGCGCGCGCTG 120
Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY  192 CGAGTCCC CGGTTTCAGCATGGGACCTCTCCGAGCAGCAGCAGCGCCCTCGCTCTCTGC 251
Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY  121 CAATTCCCGGTTTCAGCCATGGGACCTCTCCGAGCAGCAGCAGCGGCCCTCGCTCTGC 180
Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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QY  432 TATGTCCTGAGCATTGTACCAACACAGCCTGCGGCTCTGCAGCAGTTGCCCTGTGGG 491
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Db   361 TATGTCCTGAGCATTGTAC--AACACAGCCTGCGGCTCTGCAGCAGTTGCC---TGTGG 415
QY  492 ACCTTTACAGGCATGAGAAATGGCATAGAGAAATGCCATGACTGTGTAGTCAGC 543
Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   416 GACCTTACCAGGCATGATGATGGCATAGAGAA--TGCATGACTGTGTAGTCAGC 465

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Job time : 3440 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 7, 2005, 23:48:58 ; Search time 3738 Seconds  
(without alignments)  
7388.225 Million cell updates/sec

Title: US-10-663-157-3  
Perfect score: 584  
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Scoring table: IDENTITY NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

#### Database :

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2: gb.htg.\*  
3: gb.in.\*  
4: gb.om.\*  
5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pl.\*  
9: gb.pr.\*  
10: gb.ro.\*  
11: gb.sts.\*  
12: gb.sy.\*  
13: gb.un.\*  
14: gb.vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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|------------|-------|-------------|--------|----------|--------------------|
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| 2          | 578   | 99.0        | 584    | AR437901 | AR437901 Sequence  |
| 3          | 576.4 | 98.7        | 2271   | BD263012 | BD263012 Nucleic a |
| 4          | 571.6 | 97.9        | 1686   | BD263011 | BD263011 Nucleic a |
| 5          | 570   | 97.6        | 1686   | BD263014 | BD263014 Nucleic a |
| 6          | 550.2 | 94.2        | 588    | AR437902 | AR437902 Sequence  |
| 7          | 544.8 | 93.3        | 2636   | AX876881 | AX876881 Sequence  |
| 8          | 544.8 | 93.3        | 2636   | BD156366 | BD156366 Primer fo |
| 9          | 544.8 | 93.3        | 2636   | AK001504 | AK001504 Homo sapi |
| 10         | 544.8 | 93.3        | 2638   | AR134339 | AR134339 Sequence  |
| 11         | 544.8 | 93.3        | 2638   | BD076495 | BD076495 Novel mol |
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| 14         | 544.8 | 93.3        | 3474   | AR200579 | AR200579 Sequence  |
| 15         | 544.8 | 93.3        | 3474   | AR441939 | AR441939 Sequence  |
| 16         | 544.8 | 93.3        | 3474   | BD124556 | BD124556 Human tum |
| 17         | 543.2 | 93.0        | 3534   | CQ767596 | CQ767596 Sequence  |
| 18         | 543.2 | 93.0        | 3534   | AX376350 | AX376350 Sequence  |
| 19         | 543.2 | 93.0        | 3534   | AY358304 | AY358304 Homo sapi |

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| 23 | 405   | 69.3 | 3277 | 6  | BD261788  | BD261788 Tumor nec |
| 24 | 386.6 | 66.2 | 2748 | 10 | BC016420  | BC016420 Mus muscu |
| 25 | 386   | 66.1 | 773  | 6  | BD263013  | BD263013 Nucleic a |
| 26 | 386   | 66.1 | 3238 | 9  | BC017730  | BC017730 Homo sapi |
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| 28 | 381   | 65.2 | 2186 | 6  | AR437900  | AR437900 Sequence  |
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| 36 | 375   | 64.2 | 1968 | 6  | AX327471  | AX327471 Sequence  |
| 37 | 375   | 64.2 | 1968 | 6  | AX558233  | AX558233 Sequence  |
| 38 | 375   | 64.2 | 1968 | 6  | AX706993  | AX706993 Sequence  |
| 39 | 375   | 64.2 | 1968 | 9  | AF068868  | AF068868 Homo sapi |
| 40 | 375   | 64.2 | 1968 | 9  | BT007420  | BT007420 Homo sapi |
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| 43 | 302.8 | 51.8 | 2393 | 6  | BD263015  | BD263015 Nucleic a |
| 44 | 299.8 | 51.3 | 1968 | 10 | AY043489  | AY043489 Mus muscu |
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#### ALIGNMENTS

|             |  |            |       |             |                 |
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| RESULT 1    | E29453   | 584 bp     | DNA   | linear      | PAT 18-JUN-2001 |
| E29453      | Tumor necrosis-associated receptor TR7.                            |            |       |             |                 |
| LOCUS       | E29453   |            |       |             |                 |
| DEFINITION  | Tumor necrosis-associated receptor TR7.                            |            |       |             |                 |
| ACCESSION   | E29453   |            |       |             |                 |
| VERSION     | E29453.1 GI:13025565   |            |       |             |                 |
| KEYWORDS    | JP 1999018786-A/2.   |            |       |             |                 |
| SOURCE      | unidentified   |            |       |             |                 |
| ORGANISM    | unidentified   |            |       |             |                 |
| REFERENCE   | 1 (bases 1 to 584)   |            |       |             |                 |
| AUTHORS     | Keith,C.D., Mark,R.H., Peter,Y. and K.B.T.                         |            |       |             |                 |
| TITLE       | Tumor necrosis-associated receptor TR7                             |            |       |             |                 |
| JOURNAL     | Patent: JP 1999018786-A 2 26-JAN-1999;                             |            |       |             |                 |
| COMMENT     | SMITHKLINE BEECHAM CORP  |            |       |             |                 |
|             | OS Unidentified  |            |       |             |                 |
|             | PN JP 1999018786-A/2   |            |       |             |                 |
|             | PD 26-JAN-1999   |            |       |             |                 |
|             | PF 02-APR-1998 JP 1998126559                                       |            |       |             |                 |
|             | PR 02-APR-1997 US 60/041796-28-OCT-1997 US 08/959382 PI            |            |       |             |                 |
|             | KEITH C DEAN,MARK R HURLE,PETER YOUNG,K B TAN PC                   |            |       |             |                 |
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|             | A61K48/00,   |            |       |             |                 |
|             | PC C07K14/705,C07K16/30,C12N1/15,C12N1/19,C12N1/21,C12N5/10, PC    |            |       |             |                 |
|             | C12N5/10,  |            |       |             |                 |
|             | PC   |            |       |             |                 |
|             | C12P21/02,G01N33/53,G01N33/531,G01N33/566,G01N33/577,C12N15/00, PC |            |       |             |                 |
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|             | CC Topology: Linear;   |            |       |             |                 |
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Best Local Similarity 100.0%; Pred. No. 2.1e-108;
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DEFINITION Nucleic acids encoding osteoprotegerin-like proteins and methods of
using same.
ACCESSION BD263012
VERSION BD263012.1 GI:33072780
KEYWORDS JP 2002528067-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 2271)
AUTHORS Shimkets, R.A., Yang, M., Lichenstein, H. and McDonald, W.F.
TITLE Nucleic acids encoding osteoprotegerin-like proteins and methods of
using same
JOURNAL Patent: JP 2002528067-A 2 03-SEP-2002;
CURAGEN CORP
COMMENT OS Homo sapiens (human)
PN JP 2002528067-A/2
PD 03-SEP-2002
PF 22-OCT-1999 JP 2000578341
PR 23-OCT-1998 US 60/105481.01-OCT-1999 US 60/156993 PR
21-OCT-1999 US 09/422680
PI RICHARD A SHIMKETS, MEIJIA YANG, HENRI LICHENSTEIN, WILLIAM F PI
MCDONALD
PC C12N15/09, A61K31/711, A61K38/00, A61K38/22, A61K39/395, A61K45/00,
PC A61P19/00,
PC A61P19/08, A61P19/10, A61P43/00, C07K14/51, C07K16/22, C12N1/15, PC
C12N1/19,
PC C12N1/21, C12N5/10, C12P21/08, C12N15/00, C12N5/00, A61K37/02, PC
A61K37/24
CC wherein any n is an a, t, c or g
FH Key Location/Qualifiers
FT CDS (102)..(2174)
FT misc feature (3)..(37).
FT Location/Qualifiers

Query Match 99.0%; Score 578; DB 6; Length 584;
Best Local Similarity 100.0%; Pred. No. 2.1e-108;
Matches 584; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGNCCGCGNGNGNGCAAGTGCTGAGCGCCCTTAGNGCTCCCTTGGCGCTCCCTCC 60
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QY 61 TCTGCCCGGCGGTAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCGCGGGAG 120
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DEFINITION Sequence 3 from patent US 6660839.
ACCESSION AR437901
VERSION AR437901.1 GI:40203125
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 584)
AUTHORS Deen, K.C., Hurlle, M.R., Young, P. and Tan, K.B.
TITLE Tumor necrosis related receptor, FR7
JOURNAL Patent: US 6660839-A 3 09-DEC-2003;
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Best Local Similarity 100.0%; Pred. No. 2.1e-108;
Matches 584; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGNCCGCGNGNGNGCAAGTGCTGAGCGCCCTTAGNGCTCCCTTGGCGCTCCCTCC 60
DB 1 GCGNCCGCGNGNGNGCAAGTGCTGAGCGCCCTTAGNGCTCCCTTGGCGCTCCCTCC 60
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Best Local Similarity 99.8%; Pred. No. 4e-108;
Matches 583; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 121 GCGCGGTGTATCGCGCTGGGAGAGCAGCGCGGATTCAGCTGCCCGCGGGCCC 180
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DB 541 AGCCATGCCCATGGCAATGATTGAGAAATTACCTTGTGTGCC 584

RESULT 4
BD263011 1686 bp DNA linear PAT 17-JUL-2003
LOCUS Nucleic acids encoding osteoprotegerin-like proteins and methods of
DEFINITION using same.
ACCESSION BD263011
VERSION BD263011.1 GI:33072779
KEYWORDS JP 2002528067-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
TITLE Shimkets,R.A., Yang,M., Lichenstein,H. and Mcdonald,W.F.
Nucleic acids encoding osteoprotegerin-like proteins and methods of
JOURNAL Patent: JP 2002528067-A 1 03-SEP-2002;
CURAGEN CORP
COMMENT OS Homo sapiens (human)
PN JP 2002528067-A/1
PD 03-SEP-2002
PF 22-OCT-1999 JP 2000578341

PR 23-OCT-1998 US 60/105481,01-OCT-1999 US 60/156993 PR
21-OCT-1999 US 09/422680
PI RICHARD A SHIMKETS,MEIJIA YANG,HENRI LICHENSTEIN,WILLIAM F PI
MCDONALD
PC C12N15/09,A61K31/711,A61K38/00,A61K38/22,A61K39/395,A61K45/00,
PC A61P19/00,
PC A61P19/08,A61P19/10,A61P43/00,C07K14/51,C07K16/22,C12N1/15,PC
C12N1/19,
PC C12N1/21,C12N5/10,C12P21/08,C12N15/00,C12N5/00,A61K37/02,PC
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CC wherein any n is an a, t, c or g
FH Key Location/Qualifiers
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LOCUS Nucleic acids encoding osteoprotegerin-like proteins and methods of
DEFINITION using same.
ACCESSION BD263014
VERSION BD263014.1 GI:33072782
KEYWORDS JP 2002528067-A/1
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
TITLE Shimkets,R.A., Yang,M., Lichenstein,H. and Mcdonald,W.F.
Nucleic acids encoding osteoprotegerin-like proteins and methods of
JOURNAL Patent: JP 2002528067-A 1 03-SEP-2002;
CURAGEN CORP
COMMENT OS Homo sapiens (human)
PN JP 2002528067-A/1
PD 03-SEP-2002
PF 22-OCT-1999 JP 2000578341
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 REFERENCE 1 (bases 1 to 1686)  
 AUTHORS Shimkets, R.A., Yang, M., Lichenstein, H. and McDonald, W.F.  
 TITLE Nucleic acids encoding osteoprotegerin-like proteins and methods of using same  
 JOURNAL Patent: JP 2002528067-A 4 03-SEP-2002;  
 CURAGEN CORP  
 COMMENT OS Homo sapiens (human)  
 PN JP 2002528067-A/4  
 PD 03-SEP-2002  
 PP 22-OCT-1999 JP 2000578341  
 PR 23-OCT-1998 US 60/105481, 01-OCT-1999 US 60/156993 PR  
 21-OCT-1999 US 09/422680  
 PI RICHARD A SHIMKETS, MEIJIA YANG, HENRI LICHENSTEIN, WILLIAM F PI  
 McDONALD  
 PC C12N15/09, A61K31/711, A61K38/00, A61K38/22, A61K39/395, A61K45/00,  
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 methods of using

CC same  
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 DEFINITION Sequence 5 from patent US 6660839.  
 ACCESSION AR437902  
 VERSION AR437902.1 GI:40203126  
 KEYWORDS Unknown.  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 588)  
 AUTHORS Deen, K.C., Hurler, M.R., Young, P., and Tan, K.B.  
 TITLE Tumor necrosis related receptor, TR7  
 JOURNAL Patent: US 6660839-A 5 09-DEC-2003;  
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ACCESSION AX876881
VERSION    AX876881.1 GI:40031617
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
            Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
TITLE      Primers for synthesizing full-length cDNA and their use
JOURNAL    Patent: EP 1074617-A 11786 07-FEB-2001.
JOURNAL    Research Association for Biotechnology (JP)
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Query Match      93.3%; Score 544.8; DB 6; Length 2636;
Best Local Similarity 97.4%; Pred. No. 1.2e-101;
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LOCUS      2636 bp      DNA      linear      PAT 17-JAN-2003
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD156366
VERSION    BD156366.1 GI:27862124
KEYWORDS   JP 2002191363-A/11209.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
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ORIGIN
Query Match      93.3%; Score 544.8; DB 6; Length 2636;
Best Local Similarity 97.4%; Pred. No. 1.2e-101;
Matches 571; Conservative 0; Mismatches 13; Indels 2; Gaps 2;
QY      1  GCGNCCGCGNNGNGCAAGGTGCTGAGCGCCCTAGNGCCTCCCTTGGCGCTCCCTCC 60
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 QY 539 TCAGCCATGCCATGCCATGATTGAGAAATACCTTGTGCTGCC 584  
 Db 724 TCAGCCATGCCATGCCATGATTGAGAAATACCTTGTGCTGCC 769

## RESULT 9

AK001504  
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 DEFINITION to Homo sapiens TNFR-related death receptor-6 mRNA.

## ACCESSION

VERSION AK001504.1 GI:7022799

KEYWORDS oligo capping; fis (full insert sequence).

## SOURCE

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## AUTHORS

Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahara, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H., Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hiraoka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshihara, Y., Matsunawa, H., Ichihara, T., Shiohata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S., Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukumura, Y., Fujimori, Y., Komiyama, M., Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Noguchi, S., Itoh, T., Shigetani, K., Senba, T., Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T., and Sugano, S. Complete sequencing and characterization of 21,243 full-length human cDNAs

Nat. Genet. 36 (1), 40-45 (2004)

## JOURNAL

PUBLISHED 14702039

## REFERENCE

AUTHORS Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y.,

Nishikawa, T., Nagai, K., Sugano, S., Iehibashi, T., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hiraoka, S., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagahara, K., Masuho, Y., and Kanehori, K.  
 NEDO human cDNA sequencing project  
 Unpublished  
 3 (bases 1 to 2636)  
 Isogai, T. and Otsuki, T.  
 Direct Submission  
 Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)  
 NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection; Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.

## FEATURES

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 Matches 571; Conservative 0; Mismatches 13; Indels 2; Gaps 2;  
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LOCUS ARI134339
DEFINITION Sequence 22 from patent US 6194151.
ACCESSION ARI134339
VERSION ARI134339.1 GI:14123244
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2638)
AUTHORS Busfield,S.J.
TITLE Molecules of the TNF receptor superfamily and uses therefor
JOURNAL Patent: US 6194151-A 22 27-FEB-2001;
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    Best Local Similarity 97.4%; Pred. No. 1.2e-101;
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DEFINITION Novel molecules of TNF receptor super family and utilization thereof.
ACCESSION BD076495
VERSION BD076495.1 GI:22622098
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 2638)
AUTHORS Busfield,S.J.
TITLE Novel molecules of TNF receptor super family and utilization thereof
JOURNAL Patent: JP 2001517443-A 13 09-OCT-2001;
COMMENT MILLENNIUM PHARMACEUTICALS INC
OS Unidentified
PN JP 2001517443-A/13
PD 09-OCT-2001
PF 25-SEP-1998 JP 2000512955
PR 26-SEP-1997 US 08/938896,17-MAR-1998 US 09/042785 PI
SANTANHA J BUSFIELD
PC C12N15/09,C07K16/28,C12N5/10,C12P1/02,C12Q1/68,G01N33/53, PC
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CC Topology: Linear;
CC Novel molecules of TNF receptor super family and utilization thereof
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    Matches 571; Conservative 0; Mismatches 13; Indels 2; Gaps 2;
QY 1 GCGNCCGCGNNGNGCAAGGTGCTGAGCGCCCTTAGNGCCTCCCTTGGCGCTCCCTCC 60
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 LOCUS  
 DEFINITION  
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 deubiquitinations 11 and 12 (DUB11, DUB12), MD-1, MD-2 and cyclin  
 E2, and reagents and methods relating thereto.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 unclassified  
 unclassified  
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 1 (bases 1 to 2877)  
 REFERENCE  
 AUTHORS  
 Bates, E.E.M., Lebecque, S.J.E., Murphy, E.E., Mattson, J.D.,  
 Gorman, D.M., Hedrick, J.A., Wang, L., Zlotnik, A., Murgolo, N.J.,  
 Greene, J.R., Johnston, J.A., Bazan, J.F., Mahony, D. and Lees, E.M.  
 Mammalian genes HTEA, HSLJD37R and RANKL, HCC5 chemokine,  
 deubiquitinations 11 and 12 (DUB11, DUB12), MD-1, MD-2 and cyclin  
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 Patent: JP 2002519062-A 4 02-JUL-2002;  
 JOURNAL  
 COMMENT  
 SCHERING CORP  
 OS Unknown  
 PN JP 2002519062-A/4  
 PD 02-JUL-2002  
 PF 06-JUL-1999 JP 2000558207  
 PR 06-JUL-1998 US 09/110938, 13-JUL-1998 US 09/114466 PR  
 23-JUL-1998 US 60/093897, 12-AUG-1998 US 09/132968 PR  
 18-AUG-1998 US 09/136214, 11-SEP-1998 US 60/099999 PI  
 ELIZABETH ESTHER MARY BATES, SERGE J E LEBECQUE, ERIN E MURPHY, PI  
 JEANINE D MATTSON, DANIEL M GORMAN, JOSEPH  
 A HEDRICK, LUQUAN WANG,  
 FI ALBERT ZLOTNIK, NICHOLAS J MURGOLO, JONATHAN R GREENE, JAMES A  
 PI JOHNSTON,  
 PI JOSE FERNANDO BAZAN, DANIEL MAHONY, EMMA M LEES PC  
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 C07K16/24,  
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 C07K16/28, C07K16/40, C07K19/00, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC  
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 CC Description of Unknown Organism: primate  
 FH Key Location/Qualifiers  
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 Query Match 93.3%; Score 544.8; DB 6; Length 2877;  
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 Matches 571; Conservative 0; Mismatches 13; Indels 2; Gaps 2;

QY 1 GCGNCCGCGNNGNGCAAGGTGCTGAGCGCCCTAGNGCCTCCCTTGGCGCTCCCTCC 60  
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RESULT 13  
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 DEFINITION  
 Human tumor necrosis factor receptor TR9.  
 ACCESSION  
 BD271797  
 VERSION  
 BD271797.1 GI:33081565  
 KEYWORDS  
 JP 2002542771-A/1.  
 SOURCE  
 Homo sapiens (human)  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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 REFERENCE  
 AUTHORS  
 Ni, J., Gentz, R.L., Yu, G.L. and Fan, P.  
 Human tumor necrosis factor receptor TR9  
 Patent: JP 2002542771-A 1 17-DEC-2002;  
 JOURNAL  
 HUMAN GENOME SCIENCES INC  
 COMMENT  
 OS Homo sapiens (human)  
 PN JP 2002542771-A/1  
 PD 17-DEC-2002  
 PF 16-MAR-2000 JP 20000606721  
 PR 24-MAR-1999 US 60/126019, 14-MAY-1999 US 60/134220 PI  
 JIAN NI, REINER L GENTZ, GUO LIANG YU, PING FAN  
 PC C12N15/09, A61K38/00, A61K39/395, A61K45/00, A61K48/00,  
 PC A61P1/04,  
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 A61P25/00,  
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 PC A61P31/22,  
 PC A61P35/00, A61P35/02, A61P37/00, A61P37/02, C07K14/715, C07K16/28,  
 PC C12N1/15,  
 PC C12N1/19, C12N1/21, C12N5/10, C12P21/02, G01N33/15, G01N33/50, PC  
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 PC G01N33/564, G01N33/566// (C12P21/02, C12R1/19), (C12P21/02 PC  
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 CC Human tumor necrosis factor receptor TR9  
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Job time : 3743 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 7, 2005, 22:11:19 ; Search time 521 Seconds

(without alignments)

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Title: US-10-663-157-3

Perfect score: 584

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
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Listing first 45 summaries

Database :

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  - 12: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 38 | 543.2 | 93.0 | 3534 | 8 | ACD25566 | ACD25566 Novel hum |
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| 41 | 543.2 | 93.0 | 3534 | 8 | ACD21684 | ACD21684 Human sec |
| 42 | 543.2 | 93.0 | 3534 | 8 | ACD18751 | ACD18751 Human sec |
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ALIGNMENTS

RESULT 1

AAV57442

ID AAV57442 standard; cDNA; 584 BP.

AC AAV57442;

XX 21-DEC-1998 (first entry)

DT Human tumour necrosis factor related receptor TR7 cDNA fragment.

XX Tumour necrosis factor related receptor; TR7; human; inflammation;

XX arthritis; septicemia; autoimmune disease; psoriasis;

XX inflammatory bowel disease; infection; graft-versus-host disease;

XX transplant rejection; stroke; acute respiratory disease syndrome;

XX ischaemia; restenosis; brain injury; AIDS; bone disease; cancer;

XX atherosclerosis; Alzheimer's disease; diagnosis; therapy; vaccine; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 210..584

XX FT /\*tag= a

XX EP869179-A1.

XX 07-OCT-1998.

XX 01-APR-1998; 98EP-00302528.

XX 02-APR-1997; 97US-0041796P.

XX 28-OCT-1997; 97US-00959382.

XX (SMIK ) SMITHKLINE BEECHAM CORP.

XX Deen KC, Hurle MR, Young P, Tan KB;

XX WPI; 1998-508493/44.

XX P-PSDB; AAW75793.

XX New tumour necrosis factor receptor TR7 polypeptides and polynucleotides

XX - useful as diagnostic reagents and for treating Alzheimer's disease,

XX AIDS and cancer.

XX Disclosure; Page 21-22; 25pp; English.

XX

XX This cDNA clone codes for the N-terminal portion (see AAW75793) of a  
 CC novel member of the human tumour necrosis factor (TNF) receptor  
 CC superfamily, termed TR7 (see also AAW75792). TR7 polypeptides, (see  
 CC also AAW57441) are useful for diagnosing diseases or susceptibility to  
 CC diseases by identifying mutations in the TR7 gene using probes containing  
 CC the TR7 nucleotide sequence. TR7 polypeptides can be used to screen for  
 CC agonists and antagonists which bind the receptor. Gene therapy may be  
 CC used to effect endogenous TR7 polypeptide production. TR7 polypeptides  
 CC and polynucleotides can be administered directly as vaccines for  
 CC prevention of diseases. Diseases diagnosed, treated or prevented by the  
 CC above methods include: chronic and acute inflammation, arthritis,  
 CC septicemia, autoimmune diseases (e.g. inflammatory bowel disease,  
 CC psoriasis), transplant rejection, graft vs. host disease, infection,  
 CC stroke, ischaemia, acute respiratory disease syndrome, restenosis, brain  
 CC injury, AIDS, bone diseases, cancer (e.g. lymphoproliferative disorders),  
 CC atherosclerosis, and Alzheimer's disease. TR7 polynucleotides are also  
 CC useful for mapping the gene to a chromosome, allowing gene inheritance to  
 CC be studied through linkage analysis  
 XX  
 SQ Sequence 584 BP; 106 A; 200 C; 168 G; 104 T; 0 U; 6 Other;

Query Match 99.0%; Score 578; DB 2; Length 584;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-125;  
 Matches 584; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGNCCGCGGNGNGCAAGTCTGAGCGCCCTAGNGCCTCCCTGCGGCTCCCTCC 60  
 DB 1 GCGNCCGCGGNGNGCAAGTCTGAGCGCCCTAGNGCCTCCCTGCGGCTCCCTCC 60  
 QY 61 TCTGCCCGGCGTAGCAGTGCACATGGGCTGTGGAGGTAGATGGGCTCCCGCGCGGAG 120  
 DB 61 TCTGCCCGGCGTAGCAGTGCACATGGGCTGTGGAGGTAGATGGGCTCCCGCGCGGAG 120  
 QY 121 GCGGCGGTGATGCGGCGTGGGAGAGAGCAGCGCGCGATTCAGCTGCGCGCGGCC 180  
 DB 121 GCGGCGGTGATGCGGCGTGGGAGAGAGCAGCGCGCGATTCAGCTGCGCGCGGCC 180  
 QY 181 CGGCCACCTTGGCAGTCCCGGTTGAGCCATGGGACCTCTCCGAGCAGCAGCAGCC 240  
 DB 181 CGGCCACCTTGGCAGTCCCGGTTGAGCCATGGGACCTCTCCGAGCAGCAGCAGCC 240  
 QY 241 TCGCCTCTGACGCGCATCGCCGCGGAGCCACAGCAGATGATCGGGGCTCCCTTC 300  
 DB 241 TCGCCTCTGACGCGCATCGCCGCGGAGCCACAGCAGATGATCGGGGCTCCCTTC 300  
 QY 301 TCTGCTTGATTCCTTAGCACCACACAGCTCAGCCAGAACAGAGGCTCCGAATCTCA 360  
 DB 301 TCTGCTTGATTCCTTAGCACCACACAGCTCAGCCAGAACAGAGGCTCCGAATCTCA 360  
 QY 361 TTGGCACAATACCGCCATGTTGACCGTCCACCGCGGAGGCTTAACCTGTGACAAGTGC 420  
 DB 361 TTGGCACAATACCGCCATGTTGACCGTCCACCGCGGAGGCTTAACCTGTGACAAGTGC 420  
 QY 421 CAGCAGGAACCTATGCTCTGAGCATTTGTACCAACACAGCCTGCGCGTCTGAGCAGTT 480  
 DB 421 CAGCAGGAACCTATGCTCTGAGCATTTGTACCAACACAGCCTGCGCGTCTGAGCAGTT 480  
 QY 481 GCCTGTGGGACCTTTACAGGATAGAAATGGCATAGAAATGGCATAGTGTAGTC 540  
 DB 481 GCCTGTGGGACCTTTACAGGATAGAAATGGCATAGAAATGGCATAGTGTAGTC 540  
 QY 541 AGCCATGCCATGGCCATGATGAGAAATTTACCTGTGTGCTGCC 584  
 DB 541 AGCCATGCCATGGCCATGATGAGAAATTTACCTGTGTGCTGCC 584

RESULT 2

AAA28728

ID AAA28728 standard; DNA; 2271 BP.

XX

AC AAA28728;

XX

DT 29-AUG-2000 (first entry)  
 XX Human osteoprotegerin-like 2 (OPGx2) DNA.  
 DE  
 XX OPGx1; osteoprotegerin-like; DR6 TNF-related death receptor; agonist;  
 KW inhibitor; bone resorption; vascular calcification; apoptosis;  
 KW osteopathic; chromosome 6p11.1; D6S452; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 CDS 102..2177  
 FT /\*tag= a  
 FT /product= "OPGx2"  
 XX  
 FN WO200024771-A2.  
 XX  
 PD 04-MAY-2000.  
 XX  
 XX 22-OCT-1999; 99WO-US024913.  
 XX  
 XX 23-OCT-1998; 98US-0105481P.  
 PR 01-OCT-1999; 99US-0156993P.  
 PR 21-OCT-1999; 99US-00422680.  
 XX  
 XX (CURA-) CURAGEN CORP.  
 XX  
 XX Shinkets RA, Yang M, Lichenstein H, McDonald WF;  
 XX  
 XX WPI; 2000-350692/30.  
 XX P-PSDB; AAY92846.  
 XX  
 XX Nucleic acids encoding osteoprotegerin-like (OPGx) polypeptides, useful  
 PT for treating disorders associated with bone metabolism, such as  
 PT osteoporosis and osteopetrosis.  
 XX  
 XX Claim 1; Fig 2; 81pp; English.  
 XX  
 CC Osteoprotegerin-like polypeptides (OPGx) are expressed in bone, lymph  
 CC node, germinal B cells and kidney. There appear to be at least two splice  
 CC variants of this gene, a transmembrane form and an extracellular domain  
 CC form. Human OPGx1, 2 and 4 contain a 36 amino acid extension at their N-  
 CC terminal relative to the DR6 tumour necrosis factor (TNF)-related death  
 CC receptor. The OPGx gene has been mapped to chromosome 6p11.1, essentially  
 CC on top of D6S452. The OPGx polypeptides, agonists and antibodies are  
 CC useful in methods to inhibit osteoclast-mediated bone resorption or  
 CC vascular calcification and to modulate cell death (apoptosis). This is  
 CC useful for treating disorders associated with bone metabolism, such as  
 CC osteoporosis, osteopetrosis, or a condition characterized by loss of  
 CC bone, breakdown of tissue, or excessive resorption of bone tissue  
 XX  
 SQ Sequence 2271 BP; 518 A; 668 C; 611 G; 467 T; 0 U; 7 Other;

Query Match 98.7%; Score 576.4; DB 3; Length 2271;  
 Best Local Similarity 99.8%; Pred. No. 4e-125;  
 Matches 583; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCGNCCGCGGNGNGCAAGTCTGAGCGCCCTAGNGCCTCCCTGCGGCTCCCTCC 60  
 DB 1 GCGNCCGCGGNGNGCAAGTCTGAGCGCCCTAGNGCCTCCCTGCGGCTCCCTCC 60  
 QY 61 TCTGCCCGGCGTAGCAGTGCACATGGGCTGTGGAGGTAGATGGGCTCCCGCGCGGAG 120  
 DB 61 TCTGCCCGGCGTAGCAGTGCACATGGGCTGTGGAGGTAGATGGGCTCCCGCGCGGAG 120  
 QY 121 GCGGCGGTGATGCGGCGTGGGAGAGAGCAGCGCGGATTCAGTGTCCCGCGCGGCC 180  
 DB 121 GCGGCGGTGATGCGGCGTGGGAGAGAGCAGCGCGGATTCAGTGTCCCGCGCGGCC 180  
 QY 181 CGGCCACCTTGGCAGTCCCGGTTGAGCCATGGGACCTCTCCGAGCAGCAGCAGCC 240  
 DB 181 CGGCCACCTTGGCAGTCCCGGTTGAGCCATGGGACCTCTCCGAGCAGCAGCAGCC 240

Qy 241 TCGCTCTCGAGCGCATCGCCGCGAGCCACAGCCAGATGATCGCGGCTCCCTTC 300  
Dbb 241 TCGCTCTCGAGCGCATCGCCGCGAGCCACAGCCAGATGATCGCGGCTCCCTTC 300  
Qy 301 TCGCTCTCGAGCGCATCGCCGCGAGCCACAGCCAGATGATCGCGGCTCCCTTC 360  
Dbb 301 TCGCTCTCGAGCGCATCGCCGCGAGCCACAGCCAGATGATCGCGGCTCCCTTC 360  
Qy 361 TTGSCACATACCGCATGTTGACCGTGCACCGCCAGGCTGCTAACTGTGACAAAGTGC 420  
Dbb 361 TTGSCACATACCGCATGTTGACCGTGCACCGCCAGGCTGCTAACTGTGACAAAGTGC 420  
Qy 421 CAGCAGAACTATGCTCTGAGCATTTGACCAACAGCCGCGCTGCGGCTGCGAGCAGTT 480  
Dbb 421 CAGCAGAACTATGCTCTGAGCATTTGACCAACAGCCGCGCTGCGGCTGCGAGCAGTT 480  
Qy 481 GCCTGTGGGGACCTTTACGAGCATGAGATGAGAAATACCTTGTGTGCC 584  
Dbb 481 GCCTGTGGGGACCTTTACGAGCATGAGATGAGAAATACCTTGTGTGCC 584

RESULT 3

AAA28724  
ID AAA28724 standard; DNA; 1686 BP.  
XX  
AC AAA28724;  
XX  
DT 29-AUG-2000 (first entry)  
XX  
DE Human osteoprotegrin-like 1 (OPGx1) DNA.  
XX  
KW OPGx1; osteoprotegrin-like; DR6 TNF-related death receptor; agonist;  
KW inhibitor; bone resorption; vascular calcification; apoptosis;  
KW osteopathic; chromosome 6p11.1; D6S452; ss.  
XX  
OS Homo sapiens.

Key Location/Qualifiers  
CDS 102..974  
FT /\*tag= a  
FT /product= "OPGx1"  
XX  
PN WO200024771-A2.  
XX  
PD 04-MAY-2000.  
XX  
PP 22-OCT-1999; 99WO-US024913.  
XX  
PR 23-OCT-1998; 98US-0105481P.  
PR 01-OCT-1999; 99US-0156993P.  
PR 21-OCT-1999; 99US-00422680.  
XX  
PA (CURA-) CURAGEN CORP.  
XX  
PI Shimkets RA, Yang M, Lichenstein H, McDonald WP;  
XX  
XX WPI; 2000-350692/30.  
DR P-PSDB; AAY92842.  
XX

Nucleic acids encoding osteoprotegrin-like (OPGx) polypeptides, useful for treating disorders associated with bone metabolism, such as osteoporosis and osteopetrosis.  
XX  
PS Claim 1; Fig 1; 81pp; English.  
XX  
CC Osteoprotegrin-like polypeptides (OPGx) are expressed in bone, lymph node, germinal B cells and kidney. There appear to be at least two splice variants of this gene, a transmembrane form and an extracellular domain form. Human OPGx1, 2 and 4 contain a 36 amino acid extension at their N-terminus.  
XX  
CC

terminal relative to the DR6 tumour necrosis factor (TNF)-related death receptor. The OPGx gene has been mapped to chromosome 6p11.1, essentially on top of D6S452. The OPGx polypeptides, agonists and antibodies are useful in methods to inhibit osteoclast-mediated bone resorption or vascular calcification and to modulate cell death (apoptosis). This is useful for treating disorders associated with bone metabolism, such as osteoporosis, osteopetrosis, or a condition characterized by loss of bone, breakdown of tissue, or excessive resorption of bone tissue  
XX  
SQ Sequence 1686 BP; 438 A; 429 C; 408 G; 406 T; 0 U; 5 Other;  
Query Match 97.9%; Score 571.6; DB 3; Length 1686;  
Best Local Similarity 99.1%; Pred. No. 5e-124;  
Matches 579; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
Qy 1 GCNCGCCGNGNGNGCAAGGTGCTCAGCGCCCTAGNGCCTCCCTTGCCTCCCTCCCTCC 60  
Dbb 1 GCNCGCCGNGNGNGCAAGGTGCTCAGCGCCCTAGNGCCTCCCTTGCCTCCCTCCCTCC 60  
Qy 61 TCTGCCCGCGCTGAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCGCGCGGAG 120  
Dbb 61 TCTGCCCGCGCTGAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCGCGCGGAG 120  
Qy 121 GCAGCGGTGATGCGCGGCTGGGCAAGAGCGCGGATTTCCAGCTGCCCGCGCGGCC 180  
Dbb 121 GCAGCGGTGATGCGCGGCTGGGCAAGAGCGCGGATTTCCAGCTGCCCGCGCGGCC 180  
Qy 181 CGGCCACCTTGGCGAGTCCCGGTTTCCAGCATGGGACCTCTCCGAGCAGCAGCAGCCGCC 240  
Dbb 181 CGGCCACCTTGGCGAGTCCCGGTTTCCAGCATGGGACCTCTCCGAGCAGCAGCAGCCGCC 240  
Qy 241 TCGCCTCTCGAGCGCATCGCCGCGAGCCACAGCCAGATGATCGCGGCTCCCTTC 300  
Dbb 241 TCGCCTCTCGAGCGCATCGCCGCGAGCCACAGCCAGATGATCGCGGCTCCCTTC 300  
Qy 301 TCTGCTTGATTTCTTAGCACCACACAGCTCAGCCAGAACAGAGGCTTCGAATCTCA 360  
Dbb 301 TCTGCTTGATTTCTTAGCACCACACAGCTCAGCCAGAACAGAGGCTTCGAATCTCA 360  
Qy 361 TTGGCACATACCGCATGTTGACCGTGCACCGCCAGGCTGCTAACTGTGACAAAGTGC 420  
Dbb 361 TTGGCACATACCGCATGTTGACCGTGCACCGCCAGGCTGCTAACTGTGACAAAGTGC 420  
Qy 421 CAGCAGAACTATGCTCTGAGCATTTGACCAACAGCCGCTGCGGCTGCGAGCAGTT 480  
Dbb 421 CAGCAGAACTATGCTCTGAGCATTTGACCAACAGCCGCTGCGGCTGCGAGCAGTT 480  
Qy 481 GCCTGTGGGGACCTTTACGAGCATGAGATGAGAAATACCTTGTGTGCC 540  
Dbb 481 GCCTGTGGGGACCTTTACGAGCATGAGATGAGAAATACCTTGTGTGCC 540  
Qy 541 AGCCATGCCCATGGCCAAATGATTGAGAAATACCTTGTGTGCC 584  
Dbb 541 AGCCATGCCCATGGCCAAATGATTGAGAAATACCTTGTGTGCC 584

RESULT 4

AAA28726  
ID AAA28726 standard; DNA; 1686 BP.  
XX  
AC AAA28726;  
XX  
DT 29-AUG-2000 (first entry)  
XX  
DE Human osteoprotegrin-like 4 (OPGx4) DNA.  
XX  
KW OPGx4; osteoprotegrin-like; DR6 TNF-related death receptor; agonist;  
KW inhibitor; bone resorption; vascular calcification; apoptosis;  
KW osteopathic; chromosome 6p11.1; D6S452; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers

```

FT CDS 102..974
FT /*tag= a
FT /product= "OPGx4"
XX PN WO200024771-A2.
XX PD 04-MAY-2000.
XX PF 22-OCT-1999; 99WO-US024913.
XX PR 23-OCT-1998; 98US-0105481P.
XX PR 01-OCT-1999; 99US-0156993P.
XX PR 21-OCT-1999; 99US-00422680.
XX PA (CURA-) CURAGEN CORP.
XX PI Shimkets RA, Yang M, Lichenstein H, McDonald WF;
XX P-PSDB; AAY92844.
XX Nucleic acids encoding osteoprotegerin-like (OPGx) polypeptides, useful
FT for treating disorders associated with bone metabolism, such as
PT osteoporosis and osteopetrosis.
XX Claim 1; Fig 6; 81pp; English.
XX Osteoprotegerin-like polypeptides (OPGx) are expressed in bone, lymph
CC node, germinal B cells and kidney. There appear to be at least two splice
CC variants of this gene, a transmembrane form and an extracellular domain
CC form. Human OPGx1, 2 and 4 contain a 36 amino acid extension at their N-
CC terminal relative to the DR6 tumour necrosis factor (TNF)-related death
CC receptor. The OPGx gene has been mapped to chromosome 11p11, essentially
CC on top of D6S452. The OPGx polypeptides, agonists and antibodies are
CC useful in methods to inhibit osteoclast-mediated bone resorption or
CC vascular calcification and to modulate cell death (apoptosis). This is
CC useful for treating disorders associated with bone metabolism, such as
CC osteoporosis, osteopetrosis, or a condition characterized by loss of
CC bone, breakdown of tissue, or excessive readorption of bone tissue
XX SQ Sequence 1686 BP; 435 A; 428 C; 406 G; 410 T; 0 U; 7 Other;

Query Match 97.6%; Score 570; DB 3; Length 1686;
Best Local Similarity 99.0%; Pred. No. 1.2e-123;
Matches 578; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GCGNCCGCGNNGNGCAAGGTGCTGAGCGCCCTAGNGCCTCCTTTGCGGCTCCCTCC 60
DB 1 GCGNCCGCGNNGNGCAAGGTGCTGAGCGCCCTAGAGCCTCCTTTGCGGCTCCCTCC 60
QY 61 TCTGCCCGCGGTAGCGGCTGGGAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCGCGCGGAG 120
DB 61 TCTGCCCGCGGTAGCGGCTGGGAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCGCGCGGAG 120
QY 121 GCGGCGGTGATGCGGCGCTGGGAGAGCAGCGCGCGATTCAGCTGCGCCCGCGGCGCC 180
DB 121 GCGGCGGTGATGCGGCGCTGGGAGAGCAGCGCGCGATTCAGCTGCGCCCGCGGCGCC 180
QY 181 GCGGCACTTCGAGTCCCGGTTTCCGCAATGAGGACCTCTCCGAGCAGCAGCGCC 240
DB 181 GCGGCACTTCGAGTCCCGGTTTCCGCAATGAGGACCTCTCCGAGCAGCAGCAGCGCC 240
QY 241 TCGGCTCTTCAGCGGATGCGCGCGAGCGGAGCAGCGGATTCAGCTGCGCGGCTCCCTTC 300
DB 241 TCGGCTCTTCAGCGGATGCGCGCGAGCGGAGCAGCGGATTCAGCTGCGCGGCTCCCTTC 300
QY 301 TCGTCTTGGATTCCTTAGCACCACAGCTCAGCCAGCAAGAGGCGCTCGAATCTCA 360
DB 301 TCGTCTTGGATTCCTTAGCACCACAGCTCAGCCAGCAAGAGGCGCTCGAATCTCA 360
QY 361 TTGGCACAATACCGCATTTGACCGTGCACCGGCGAGGCTGCTAACCTGTGACAGTGC 420
DB 361 TTGGCACAATACCGCATTTGACCGTGCACCGGCGAGGCTGCTAACCTGTGACAGTGC 420

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421 CAGCAGGAACCTATGCTCTGAGCATTTGACCAACACAGCTGCGCTCTGCACAGTT 480

421 CAGCAGGAACCTATGCTCTGAGCATTTGACCAACACAGCTGCGCTCTGCACAGTT 480

481 GCCCTGTGGGACCTTTTACCAGGCATGAGAAATGCGATAGAGAAATGCCATGACTAGTC 540

481 GCCCTGTGGGACCTTTTACCAGGCATGAGAAATGCGATAGAGAAATGCCATGACTAGTC 540

541 AGCCATGCCCATGGCCAAATGATTGAGAAATTACCTTTGTGCTGCC 584

541 AGCCATGCCCATGGCCAAATGATTGAGAAATTACCTTTGTGCTGCC 584

RESULT 5

AA25260

ID AAX25260 standard; cDNA; 2646 BP.

XX AC AAX25260;

XX 19-JUL-1999 (first entry)

XX Human soluble tumour necrosis factor receptor ZTNFR-6 cDNA.

XX ZTNFR-6; tumour necrosis factor receptor-6; human; cell maturation;

XX bone cell regulation; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 284..973

XX FT /\*tag= a

XX FT /product= "soluble ZTNFR-6"

XX FT /note= "this region of the sequence is specifically

XX FT claimed in Claim 10(b)"

XX FT 284..334

XX FT sig\_peptide

XX FT /\*tag= b

XX FT mat\_peptide 335..973

XX FT /\*tag= c

XX WO9911790-A1.

XX 11-MAR-1999.

XX 03-SEP-1998; 98WO-US018364.

XX 04-SEP-1997; 97US-0057608P.

XX 04-SEP-1997; 97US-00923725.

XX (ZYMO ) ZYMOGENETICS INC.

XX Farrah TM, Gross JA, Matthews SM;

XX WPI; 1999-205190/17.

XX P-PSDB; AAY05679.

XX New secreted or membrane bound tumor necrosis factor receptor ZTNFR-6 -

XX useful for detecting a genetic abnormality in a patient.

XX Claim 11a; Page 115-117; 145pp; English.

XX This is the DNA sequence of an isolated polynucleotide that codes for a

XX novel human soluble tumour necrosis factor receptor, designated ZTNFR-6

XX (see AAY05679). The polynucleotide was initially identified by querying

XX an EST database for sequences homologous to conserved motifs within the

XX TNFR family. A second clone (see AAX25279) encodes a membrane-bound ZTNFR

XX -6 (see AAY05678); it includes a 40 bp exon (see AAX25262) that puts the

XX sequence in frame for the transmembrane and cytoplasmic domains of

XX membrane-bound ZTNFR-6. The human ZTNFR-6 gene was localised to 6p21.1.

XX The isolated polynucleotides can be utilised in the recombinant

XX production of ZTNFR-6 polypeptides, and also in a claimed method for

XX detecting a genetic abnormality in a patient. ZTNFR-6 polypeptides are

XX useful in methods that promote cellular maturation and bone cell



XX AAX25259;  
 AC  
 XX  
 DT 19-JUL-1999 (first entry)  
 XX  
 DE Human full-length tumour necrosis factor receptor ZTNFR-6 cDNA.  
 XX  
 KW ZTNFR-6; tumour necrosis factor receptor-6; human; cell maturation;  
 KW bone cell regulation; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX  
 FH Key Location/Qualifiers  
 FT misc\_feature 284..2225  
 FT /tag= b  
 FT /note= "this region of the sequence is specifically  
 FT claimed in Claim 10(a)"  
 FT  
 FT CDS 284..2179  
 FT /tag= a  
 FT /product= "membrane-bound ZTNFR-6"  
 FT sig\_peptide 284..334  
 FT /tag= c  
 FT mat\_peptide 335..2176  
 FT /tag= d  
 FT  
 XX WO9911790-A1.  
 XX  
 PD 11-MAR-1999.  
 XX  
 XX 03-SEP-1998; 98WO-US018364.  
 XX  
 XX 04-SEP-1997; 97US-0057608P.  
 PR 04-SEP-1997; 97US-00923725.  
 XX  
 XX (ZYMO ) ZYMOGENETICS INC.  
 XX  
 XX Farrah TM, Gross JA, Matthews SM;  
 XX  
 XX WPI; 1999-205190/17.  
 DR P-PSDB; AAY05678.  
 DR  
 XX  
 XX New secreted or membrane bound tumor necrosis factor receptor ZTNFR-6 -  
 PT useful for detecting a genetic abnormality in a patient.  
 PT  
 XX  
 XX Claim 10a; Page 108-113; 145pp; English.  
 XX  
 CC This is the DNA sequence of an isolated polynucleotide that codes for a  
 CC novel human full-length membrane-bound tumour necrosis factor receptor,  
 CC designated ZTNFR-6 (see AAY05678). The polynucleotide was initially  
 CC identified by querying an EST database for sequences homologous to  
 CC conserved motifs within the TNFR family. A second clone (see AAX25260)  
 CC encodes truncated, soluble ZTNFR-6 (see AAY05679). The full-length clone  
 CC includes a 40 bp exon (see AAX25262) that puts the sequence in frame for  
 CC the transmembrane and cytoplasmic domains of membrane-bound ZTNFR-6. The  
 CC human ZTNFR-6 gene was localised to 6p21.1. The isolated polynucleotides  
 CC can be utilised in the recombinant production of ZTNFR-6 polypeptides,  
 CC and also in a claimed method for detecting a genetic abnormality in a  
 CC patient. ZTNFR-6 polypeptides are useful in methods that promote cellular  
 CC maturation and bone cell regulation  
 XX  
 SQ Sequence 3440 BP; 827 A; 876 C; 833 G; 904 T; 0 U; 0 Other;  
 Query Match 93.68; Score 546.4; DB 2; Length 3440;  
 Best Local Similarity 97.67; Pred. No. 4.4e-118;  
 Matches 572; Conservative 0; Mismatches 12; Indels 2; Gaps 2;  
 QY 1 GCGGCCCGGNGNGCAAGTGTGAGCGCCCTAGNGCTCCCTTGGCGCTCCCTCC 60  
 DB 1 GCGGCCCGCGCTGGCGAGGTGTGAGCGCCCTAGAGCTCCCTTGGCGCTCCCTCC 60  
 QY 61 TCTGCCCGCGGTAGAGTGCACATGGGGTGTTCGAGGTAGATGGGCTCCCGG-CCGGGA 119  
 DB 61 TCTGCCCGCGGTAGAGTGCACATGGGGTGTTCGAGGTAGATGGGCTCCCGCGCCGGGA 120

QY 120 GCGCGCGTGGATGCGGCGCTGGGCGAGAGCAGCGCGGATTCCAGCTGCCCGCGCGCC 179  
 DB 121 GCGCGCGTGGATGCGGCGCTGGGCGAGAGCAGCGCGGATTCCAGCTGCCCGCGCGCC 180  
 QY 180 CC-GGCCACCTTTGCGAGTCCCGGTTTCAGCCATGGGACCTCTCCGAGCAGCAGCACCGC 238  
 DB 181 CGGGCGCGCTTGGAGTCCCGGTTTCAGCCATGGGACCTCTCCGAGCAGCAGCACCGC 240  
 QY 239 CCTCGCTCTTCGAGCGCATGCGCGCGGAGCAGCAGCAGCAGTATCGGGGCTCCCT 298  
 DB 241 CCTCGCTCTTCGAGCGCATGCGCGCGGAGCAGCAGCAGCAGTATCGGGGCTCCCT 300  
 QY 299 TCTCTGCTTGGATTCTTAGCACCACACAGCTCAGCAGCAGAAAGAGGCTCCAACT 358  
 DB 301 TCTCTGCTTGGATTCTTAGCACCACACAGCTCAGCAGCAGAAAGAGGCTCCAACT 360  
 QY 359 CATTTGCCACATACCGCCATGTTGACCGTGCCACCGCCAGGTGCTTAACCTGTGACAAGTG 418  
 DB 361 CATTTGCCACATACCGCCATGTTGACCGTGCCACCGCCAGGTGCTTAACCTGTGACAAGTG 420  
 QY 419 TCCAGCAGAACCTATGTCTCTGAGCATTTACCAACAAGCCCTGCGGGTCTGCAGCAG 478  
 DB 421 TCCAGCAGAACCTATGTCTCTGAGCATTTACCAACAAGCCCTGCGGGTCTGCAGCAG 480  
 QY 479 TTGCGCTTGGGGACCTTTACCAGCATGAGAAATGGCATAGAGAAATGCCATGACTGTAG 538  
 DB 481 TTGCGCTTGGGGACCTTTACCAGCATGAGAAATGGCATAGAGAAATGCCATGACTGTAG 540  
 QY 539 TCAGCCATGCCCATGCCCAATGATTGAGAAATTTACCTTTGTGTGCC 584  
 DB 541 TCAGCCATGCCCATGCCCAATGATTGAGAAATTTACCTTTGTGTGCC 586

## RESULT 8

AHH14374  
 ID AHH14374 standard; cDNA; 2636 BP.  
 XX  
 AC AHH14374;  
 XX  
 DT 26-JUN-2001 (first entry)  
 XX  
 DE Human cDNA sequence SEQ ID NO:11786.  
 XX  
 KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1074617-A2.  
 XX  
 PD 07-FEB-2001.  
 XX  
 PF 28-JUL-2000; 2000EP-00116126.  
 XX  
 PR 29-JUL-1999; 99JP-00248036.  
 PR 27-AUG-1999; 99JP-00300253.  
 PR 11-JAN-2000; 2000JP-00118776.  
 PR 02-MAY-2000; 2000JP-00183767.  
 PR 09-JUN-2000; 2000JP-00241899.  
 XX  
 XX (HELI-) HELIX RES INST.  
 XX  
 XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;  
 DR WPI; 2001-318749/34.  
 XX  
 XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-  
 PT length cDNAs defined in the specification, and for the detection and/or  
 PT diagnosis of the abnormality of the proteins encoded by the full-length  
 PT cDNAs.  
 XX  
 PS Claim 8; SEQ ID NO 11786; 2537pp + Sequence Listing; English.

XX The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.

XX Sequence 2636 BP; 569 A; 762 C; 722 G; 583 T; 0 U; 0 Other;

Query Match 93.3%; Score 544.8; DB 4; Length 2636;  
Best Local Similarity 97.4%; Pred. No. 1e-117;  
Matches 571; Conservative 0; Mismatches 13; Indels 2; Gaps 2;

QY 1 GCGGCCGCGNNGNGCAAGTGCTGAGCGCCCTAGNGCCTCCCTTGGCGCTCCCTCC 60  
DB 184 GCGGCCGCGCGCTGGGAGGTGCTGAGCGCCCTAGAGCCTCCCTTGGCGCTCCCTCC 243  
QY 61 TCTGCCGCGCGTAGACATGACATGGGTGTTGGAGGTAGTGGGCTCCCGG-CGGGGA 119  
DB 244 TCTGCCGCGCGCGTAGACATGACATGGGTGTTGGAGGTAGTGGGCTCCCGGCGCGGA 303  
QY 120 GCGCGCGGTGGATGCGCGCTGGGAGAGCAGCAGCCGCGGATCCAGCTGCCCGCGGCC 179  
DB 304 GCGCGCGGTGGATGCGCGCTGGGAGAGCAGCAGCCGCGGATCCAGCTGCCCGCGGCC 363  
QY 180 CC-GGGCACCTTGGAGTCTCCCGGTTCAGCCATGGGACCTCTCCGAGCAGCAGCACCGC 238  
DB 364 CCGGGCGCCCTGGAGTCTCCCGGTTCAGCCATGGGACCTCTCCGAGCAGCAGCACCGC 423  
QY 239 CTTGCGCTCTCGAGCGCATGCGCGCCGAGCCAGCCAGCCAGCATGATGATGCGGGTCCCT 298  
DB 424 CTTGCGCTCTCGAGCGCATGCGCGCCGAGCCAGCCAGCATGATGATGCGGGTCCCT 483  
QY 299 TCTCCTGTTGGATTCCTTAGCACCACACAGCTCAGCCAGACAGAGGCTCGAATCT 358  
DB 484 TCTCCTGTTGGATTCCTTAGCACCACACAGCTCAGCCAGACAGAGGCTCGAATCT 543  
QY 359 CATTTGGACATACCGCATGTTACCGTGCACCGCGGAGGTCTAACCTGTGACAAAGTG 418  
DB 544 CATTTGGACATACCGCATGTTACCGTGCACCGCGGAGGTCTAACCTGTGACAAAGTG 603  
QY 419 TCCAGCAGGAACCTATGTTCTGAGCATTTGTACCAACAGGCTCGCGCTCTGACGAG 478  
DB 604 TCCAGCAGGAACCTATGTTCTGAGCATTTGTACCAACAGGCTCGCGCTCTGACGAG 663  
QY 479 TTGCGCTGTGGGACCTTTTACCGCATGAGATGGCATGAGAAATGCCATGCTGTAG 538  
DB 664 TTGCGCTGTGGGACCTTTTACCGCATGAGATGGCATGAGAAATGCCATGCTGTAG 723  
QY 539 TCAGCATGCGCATGGCAATGATTGAGAAATACCTTTGCTGCC 584  
DB 724 TCAGCATGCGCATGGCAATGATTGAGAAATACCTTTGCTGCC 769

ID XX AAX25322 standard; cDNA; 2638 BP.  
XX AAX25322;  
DT 19-JUL-1999 (first entry)  
XX Human TNF receptor TRL II cDNA.  
DE TRL II; TNF receptor-like; tumour necrosis factor receptor; human;  
XX signal transduction; cell differentiation; prostate cancer; inflammation;  
KW arthritis; diabetes; insulin resistance; diagnosis; therapy; ss.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FH CDS 510..2327  
FT /\*tag= a  
FT sig\_peptide 510..632  
FT mat\_peptide 633..2324  
XX WO9915663-A1.  
XX 01-APR-1999.  
XX 25-SEP-1998; 98WO-US020219.  
XX 26-SEP-1997; 97US-00938896.  
XX 17-MAR-1998; 98US-00042785.  
XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
XX Busfield SJ;  
XX WPI; 1999-254712/21.  
XX P-PSDB; AAY05697.  
XX Nucleic acid encoding tumor necrosis factor receptor-like protein.  
XX Claim 1b; Page 148-153; 170pp; English.  
CC This cDNA sequence codes for a novel member of the human tumour necrosis factor receptor superfamily (see AAY05697), termed TRL II (TNF receptor-like). A plasmid containing the full-length nucleotide sequence encoding human TRL II (clone eph75L) is deposited as ATCC 98649. TRL II has a mol.wt. of 66.2 kDa. It is a membrane-bound protein that has 4 cysteine-rich domains and a C-terminal death domain (see AAY05698). TRL II cDNA was isolated from a HeLa cDNA library using mouse TRL cDNA (see AAX25320) as probe. An alternatively spliced, secreted form, human TRL I (see AAX25321), has also been identified. Chromosomal mapping located the TRL gene on chromosome 6p25. The invention provides full-length TRL proteins, TRL fusion proteins, antigenic peptides and anti-TRL antibodies, as well as TRL nucleic acids, recombinant expression vectors, host cells and non-human transgenic animals. TRL are regulators or modulators of cellular signal transduction, cellular proliferation or differentiation, cell survival and apoptosis, immune system cells, and cells involved in insulin resistance or the diabetic response. They can be used to isolate cognate ligands, to modulate ligand/TRL interactions, to screen for potential modulators, and to treat conditions associated with abnormal TRL levels. TRL nucleic acids are used for recombinant production of TRL, to detect mutations, to identify TRL homologues, as antisense, triplex-forming or ribozyme therapeutics, for chromosome mapping and for forensic identification of individuals. Antibodies, antisense sequences, TRL protein mutants etc. that modulate activity of TRL are used to treat or prevent conditions associated with aberrant TRL protein or expression, e.g. cell proliferation and differentiation disorders (particularly cancer, especially of the prostate), inflammation (e.g. arthritis) and metabolic disease (e.g. diabetes and insulin resistance)

Query Match 93.3%; Score 544.8; DB 2; Length 2638;  
Sequence 2638 BP; 625 A; 749 C; 701 G; 563 T; 0 U; 0 Other;



Qy 299 TCTCTGCTGGATTCTTACACACACAGCTCAGCCAGAACAGAGGCTCGAATCT 358  
 Db 499 TCTCTGCTGGATTCTTACACACACAGCTCAGCCAGAACAGAGGCTCGAATCT 558  
 Qy 359 CATTTGGCACATACCGCCATGTTGACCTGCGCCAGCGGCTGTAACCTGTGACAAGTG 418  
 Db 559 CATTTGGCACATACCGCCATGTTGACCTGCGCCAGCGGCTGTAACCTGTGACAAGTG 618  
 Qy 419 TCCAGCAGGAACTATGCTCTGAGCATTTGTACCAACAAGCCCTGGCGCTGTGCACAG 478  
 Db 619 TCCAGCAGGAACTATGCTCTGAGCATTTGTACCAACAAGCCCTGGCGCTGTGCACAG 678  
 Qy 479 TTGCCCTGTGGGACCTTTACCCAGCATGGAATGGAATAATACCTTGCTGCC 538  
 Db 679 TTGCCCTGTGGGACCTTTACCCAGCATGGAATGGAATAATACCTTGCTGCC 738  
 Qy 539 TCAGCCATGCCATGGCCATGATTGAGAAATACCTTGCTGCC 584  
 Db 739 TCAGCCATGCCATGGCCATGATTGAGAAATACCTTGCTGCC 784

## RESULT 11

AAL53945  
 ID AAL53945 standard; DNA; 2877 BP.

XX AC AAL53945;

XX AC AAL53945;

XX 18-FEB-2003 (first entry)

XX 2877nt long primate DNA sequence.

XX Cytostatic; dermatological; antiinflammatory; immunosuppressive;  
 KW antigenic; forensic analysis; abnormal physiology; autoimmune disorder;  
 KW development; abnormal proliferation; cancerous; degenerative;  
 KW systemic lupus erythematosus; inflammation; chromosomal mapping;  
 KW drug screening; gene therapy; gene; ds.

XX Primates.

XX Key Location/Qualifiers  
 XX CDS 410..2377

FT FT /\*tag= b /product= "655 long primate protein"

FT FT 410..532

FT FT /\*tag= a

FT mat\_peptide 533..2374

FT FT /\*tag= c

XX US2002143147-A1.

XX 03-OCT-2002.

XX 23-APR-2001; 2001US-00840795.

XX 13-JUL-1998; 98US-0092658P.

XX 23-JUL-1998; 98US-0093897P.

XX 11-SEP-1998; 98US-0099999P.

XX 12-JUL-1999; 99US-00351777.

XX (MURP/) MURPHY E E.

XX (MATT/) MATTSON J D.

XX (BATE/) BATES E E M.

XX (GORM/) GORMAN D M.

XX (LEBE/) LEBECQUE S J E.

XX Murphy EE, Mattson JD, Bates EEM, Gorman DM, Lebecque SJE;

XX WPI: 2003-102547/09.

XX P-PSDB; AAO26523.

XX New isolated or recombinant polynucleotide encoding an antigenic

XX polypeptide, e.g. HDTBA84, HSLJD37R or RANKL polypeptide, useful for

XX

XX

XX

XX

XX

XX

XX

XX

XX

PT regulating activation, development, differentiation and function of  
 PT various cells types.

XX Claim 3; Page 33-36; 51pp; English.

XX The invention relates to an isolated or recombinant polynucleotide  
 CC encoding an antigenic polypeptide comprising at least 17 contiguous amino  
 CC acids from the mature polypeptide from a sequence having 300, 210, 655,  
 CC 444 or 150 amino acids fully defined in the specification, or from the  
 CC polypeptide from a sequence having 132, 77 or 231 amino acids given in  
 CC the specification. The polynucleotide is useful in forensic analysis,  
 CC e.g. to identify species or to separate different cell subsets or types.  
 CC The polynucleotide, polypeptide or antibody may also be used in  
 CC regulating activation, development, differentiation and function of  
 CC various cell types, including haematopoietic cells, or in diagnosing or  
 CC treating conditions associated with abnormal physiology or development,  
 CC including abnormal proliferation, e.g. in cancerous, degenerative or  
 CC autoimmune disorders (such as systemic lupus erythematosus or  
 CC inflammation). They are also useful in drug screening assays and  
 CC chromosomal mapping. The polynucleotide sequences of the invention can be  
 CC used in gene therapy to treat disorders. This polynucleotide sequence  
 CC represents a 2877nt long primate DNA relating to the antigenic proteins  
 CC of the invention

XX SQ Sequence 2877 BP; 636 A; 817 C; 751 G; 673 T; 0 U; 0 Other;

Query Match 93.3%; Score 544.8; DB 8; Length 2877;

Best Local Similarity 97.4%; Pred. No. 1e-117;

Matches 571; Conservative 0; Mismatches 13; Indels 2; Gaps 2;

Qy 1 GCGNCCGCGNNGNGCAAGGTCTGAGCGCCCTAGNGCCTCCCTTGGCGCTCCCTCC 60

Db 199 GCGCGCGCGCGCTGGCAGGTCTGAGCGCCCTAGCGCTCCCTTGGCGCTCCCTCC 258

Qy 61 TCTGCCCGCGCTGAGCATGTCACATGGGGTGTGGAGGTAGATGGCTCCGG-CCGGGA 119

Db 259 TCTGCCCGCGCGCAGCAGTGCACATGGGGTGTGGAGGTAGATGGCTCCGGCGCGGGA 318

Qy 120 GCGCGCGGTGGATGCGCGCTGGGCGAGACGACCGCCGATTCCAGCTGCCCGCGGCG 179

Db 319 GCGCGCGGTGGATGCGCGCTGGGCGAGACGACCGCCGATTCCAGCTGCCCGCGGCG 378

Qy 180 CC-GGCGACCTTGGCAGTCCCGGTTTCAGCCATGGGGACCTCTCCGAGCAGCAGCACCGC 238

Db 379 CCGGCGCGCTTGGAGTCCCGGTTTCAGCCATGGGGACCTCTCCGAGCAGCAGCACCGC 438

Qy 239 CCTGGCTCTCTGCGCGCATTCGCGCGCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 298

Db 439 CCTGGCTCTCTGCGCGCATTCGCGCGCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 498

Qy 299 TCTCTGCTTGGATTCTTACGACACACAGCTCAGCCAGCCAGCCAGCCAGCCAGCCAG 358

Db 499 TCTCTGCTTGGATTCTTACGACACACAGCTCAGCCAGCCAGCCAGCCAGCCAGCCAG 558

Qy 359 CATTTGGCACATACCGCCATGTTGACCTGCGCCAGCGGCTGTAACCTGTGACAAGTG 418

Db 559 CATTTGGCACATACCGCCATGTTGACCTGCGCCAGCGGCTGTAACCTGTGACAAGTG 618

Qy 419 TCCAGCAGGAACTATGCTCTGAGCATTTGTACCAACAAGCCCTGGCGCTGTGCACAG 478

Db 619 TCCAGCAGGAACTATGCTCTGAGCATTTGTACCAACAAGCCCTGGCGCTGTGCACAG 678

Qy 479 TTGCCCTGTGGGACCTTTACCCAGCATGGAATGGAATAATACCTTGCTGCC 538

Db 679 TTGCCCTGTGGGACCTTTACCCAGCATGGAATGGAATAATACCTTGCTGCC 738

Qy 539 TCAGCCATGCCATGGCCATGATTGAGAAATACCTTGCTGCC 584

Db 739 TCAGCCATGCCATGGCCATGATTGAGAAATACCTTGCTGCC 784

RESULT 12  
 AAV99927

ID AAV99927 standard; DNA; 3474 BP.  
XX  
AC AAV99927;  
XX  
XT 10-MAY-1999 (first entry)  
XX  
DE Novel human tumor necrosis factor receptor TR9.  
XX  
DE Human; tumour necrosis factor receptor; TNFR; TR9 receptor; cancer;  
KW apoptosis; agonist; inhibition; autoimmune disorder; viral infection;  
KW inflammation; antagonist; AIDS; neurodegenerative disorder; ss.  
XX  
OS Homo sapiens.  
XX  
PH Key Location/Qualifiers  
FT CDS 247..2214  
FT /\*tag= a  
FT /product= "human TR9 receptor"  
FT sig\_peptide 247..366  
FT /\*tag= b  
FT mat\_peptide 367..2211  
FT /\*tag= c  
XX  
PN WO9856892-A1.  
XX  
PD 17-DEC-1998.  
XX  
PF 10-JUN-1998; 98WO-US011932.  
XX  
PR 11-JUN-1997; 97US-0052991P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Ni J, Yu G, Fan P, Gentz RL;  
XX  
DR WPI; 1999-060325/05.  
DR P-PSDB; AAW81059.  
XX  
PT New isolated tumour necrosis factor-like receptor, TR9 - used to develop  
PT products for treating e.g. cancers, autoimmune disorders, viral  
PT infections, inflammation, graft rejection, neurodegenerative disorders or  
PT ischaemic injury.  
XX  
PS Claim 2; Fig 1; 134pp; English.  
XX  
CC This is the nucleotide sequence of the human tumour necrosis factor  
CC receptor (TNFR), TR9 receptor, used in the method of the invention to  
CC develop products to treat disorders such as cancers. The novel TNFR, TR9,  
CC can be used to identify agents for modifying apoptosis. Agonists can be  
CC used to treat diseases associated with increased cell survival, or the  
CC inhibition of apoptosis, including cancers (e.g. follicular lymphomas,  
CC carcinomas with p53 mutations, and hormone-dependent tumours, such as  
CC breast cancer, prostate cancer, Kaposi's sarcoma and ovarian cancer),  
CC autoimmune disorders (e.g. systemic lupus erythematosus and immune-  
CC related glomerulonephritis rheumatoid arthritis), viral infections (e.g.  
CC herpes viruses, pox viruses and adenoviruses), inflammation, graft vs  
CC host disease, acute graft rejection and chronic graft rejection.  
CC Antagonists can be used to treat diseases associated with increased  
CC apoptosis including AIDS, neurodegenerative disorders (e.g. Alzheimer's  
CC disease, Parkinson's disease, amyotrophic lateral sclerosis, retinitis  
CC pigmentosa, cerebellar degeneration), myelodysplastic syndromes (e.g.  
CC aplastic anemia), ischaemic injury (e.g. that caused by myocardial  
CC infarction, stroke and reperfusion injury), toxin-induced liver disease  
CC (e.g. that caused by alcohol), septic shock, cachexia, anorexia,  
CC inflammatory diseases and stress response related diseases, such as  
CC inflammatory bowel disease, rheumatoid arthritis, osteoarthritis,  
CC psoriasis and septicemia. The products can also be used for detection and  
CC diagnosis  
XX  
SQ Sequence 3474 BP; 832 A; 895 C; 844 G; 903 T; 0 U; 0 Other;

Query Match 93.3%; Score 544.8; DB 2; Length 3474;  
Best Local Similarity 97.4%; Pred. No. 1e-117;

Matches 571; Conservative 0; Mismatches 13; Indels 2; Gaps 2;  
QY 1 GCGNCGGNGNGCAAGGTGCTGAGCGCCCTAGNCCCTCCCTTGCGGCTCCCTCC 60  
DB |||||  
QY 36 GCGGCGGCGCGCTGGGAGGTGCTGAGCGCCCTAGAGCCCTCCCTTGCGGCTCCCTCC 95  
DB |||||  
QY 61 TCTGCCGCGCGCTAGCAGTGACATGGGGTGTGGAGGTAGATGGGCTCCCGG-CGGGA 119  
DB |||||  
QY 96 TCTGCCGCGCGCGCAGCAGTGACATGGGGTGTGGAGGTAGATGGGCTCCCGCGCGGA 155  
DB |||||  
QY 120 GCGGCGGTGGATGCGGCGCTGGGAGAGCAGCGCGGATTCAGCTGCCCGCGCGCC 179  
DB |||||  
QY 156 GCGGCGGTGGATGCGGCGCTGGGAGAGCAGCGCGGATTCAGCTGCCCGCGCGCC 215  
DB |||||  
QY 180 CC-GGCCACCTTGCGAGTCCCGGTTCCAGCCATGGGGACCTCTCCGAGCAGCAGCACCGC 238  
DB |||||  
QY 216 CCGGCGGCGCGCTGCGAGTCCCGGTTCCAGCCATGGGGACCTCTCCGAGCAGCAGCACCGC 275  
DB |||||  
QY 239 CCTCGCTCTCTGAGCGCGCATCGCCCGCGGAGCCACAGCAGATGATCGCGGCTCCCT 298  
DB |||||  
QY 276 CCTCGCTCTCTGAGCGCGCATCGCCCGCGGAGCCACAGCAGATGATCGCGGCTCCCT 335  
DB |||||  
QY 299 TCTCTGTGTGATTCCTTAGCACCAACAGCTCAGCAGAACAGAGCCCTCGAATCT 358  
DB |||||  
QY 336 TCTCTGTGTGATTCCTTAGCACCAACAGCTCAGCAGAACAGAGCCCTCGAATCT 395  
DB |||||  
QY 359 CATTGGCACATACCGCCATGTTGACCGTCCACCGCGCAGGTGCTAACTGTGACAAGTG 418  
DB |||||  
QY 396 CATTGGCACATACCGCCATGTTGACCGTCCACCGCGCAGGTGCTAACTGTGACAAGTG 455  
DB |||||  
QY 419 TCCAGCAGGAACCTATGCTCTGAGCATTTGTACCAACAGCCCTGCGGCTTCGACGAG 478  
DB |||||  
QY 456 TCCAGCAGGAACCTATGCTCTGAGCATTTGTACCAACAGCCCTGCGGCTTCGACGAG 515  
DB |||||  
QY 479 TTGCGCTGTGGGACCTTTACAGCAGTGAAGTGGCATAGAGAAATGCCATGCTGTAG 538  
DB |||||  
QY 516 TTGCGCTGTGGGACCTTTACAGCAGTGAAGTGGCATAGAGAAATGCCATGCTGTAG 575  
DB |||||  
QY 539 TCAGCCATGCCCATGCCCAATGATTGAGAAATTTACCTTGCTGTGCC 584  
DB |||||  
QY 576 TCAGCCATGCCCATGCCCAATGATTGAGAAATTTACCTTGCTGTGCC 621  
DB |||||

RESULT 13

AA99658  
ID AAA99658 standard; cDNA; 3474 BP.

XX AC AAA99658;

XX DT 02-FEB-2001 (first entry)

XX DE Human tumour necrosis factor receptor TR9 cDNA.

XX KW Human; tumour necrosis factor; TR9 receptor; immunosuppressive;  
KW antiinflammatory; cardiac; antiaesthetic; antidiabetic; antiallergic;  
KW antithalamic; antirheumatic; anti-HIV; anticonvulsant; cytostatic;  
KW neuroprotective; gene therapy; Death Domain Containing Receptor 6;  
KW common variable immunodeficiency; X-linked agammaglobulinaemia;  
KW severe combined immunodeficiency; Wiskott-Aldrich syndrome;  
KW autoimmune disease; rheumatoid arthritis; allergic encephalomyelitis;  
KW multiple sclerosis; diabetes mellitus; asthma; epilepsy; cancer;  
KW cardiovascular disease; neurological disease; protein coordinate data;  
XX ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT CDS 247..2214

XX FT /\*tag= a "TR9 receptor"

XX FT /product= 247..366

XX FT sig\_peptide /\*tag= b

XX FT mat\_peptide 367..2214

PT XX FT  
 PN XX PN  
 XX XX  
 XX XX  
 PD XX  
 XX XX  
 PF XX  
 XX XX  
 XX XX  
 PR XX  
 PR XX  
 XX XX  
 XX XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX Ni J, Gentz RL, Yu G, Fan P;  
 XX WPI; 2000-594575/56.  
 DR P-PSDB; AAB26981.  
 DR XX  
 XX Nucleic acid molecule encoding a human tumor necrosis factor receptor,  
 PT known as TR9, useful for treating, preventing and diagnosing severe  
 PT combined immunodeficiency, autoimmune diseases, HIV infection, epilepsy  
 PT and cancer.  
 XX  
 XX Claim 2; Fig 1; 220pp; English.  
 XX  
 CC The present sequence encodes a novel human tumour necrosis factor  
 CC receptor, designated TR9. The TR9 receptor is also known as Death Domain  
 CC Containing Receptor 6. TR9 polypeptides, polynucleotides or agonists are  
 CC useful for treating, preventing or diagnosing common variable  
 CC immunodeficiency, X-linked agammaglobulinemia, severe combined  
 CC immunodeficiency and Wiskott-Aldrich syndrome, autoimmune diseases (such  
 CC as rheumatoid arthritis, allergic encephalomyelitis, multiple sclerosis,  
 CC diabetes mellitus and asthma), HIV infection, epilepsy, cancer,  
 CC cardiovascular diseases and other neurological diseases  
 XX  
 SQ Sequence 3474 BP; 832 A; 895 C; 844 G; 903 T; 0 U; 0 Other;  
 Query Match 93.3%; Score 544.8; DB 3; Length 3474;  
 Best Local Similarity 97.4%; Pred. No. 1e-117;  
 Matches 571; Conservative 0; Mismatches 13; Indels 2; Gaps 2;  
 QY 1 GCGNCCGCGGNGNGCAAGGTGCTAGCGCCCTAGNGCCTCTCTTGGCGCTCCCTCC 60  
 DB 36 GCGGCGCGCGCTGCGGCGAGGTGCTAGCGCCCTAGAGCCTCTCTTGGCGCTCCCTCC 95  
 QY 61 TCTGCCCGCGGTAGCATGCATGGGTTGGAGTAGTGGCTCCCG-CCGGGA 119  
 DB 96 TCTGCCCGCGCGGAGCATGCATGGGTTGGAGTAGTGGCTCCCGCGCGCGGA 155  
 QY 120 GCGGCGCGGTGGATGCGGCGCTGGGCGAGAGCAGCGCGCGATTCAGCTGCCCGCGCGCC 179  
 DB 156 GCGGCGCGGTGGATGCGGCGCTGGGCGAGAGCAGCGCGCGATTCAGCTGCCCGCGCGCC 215  
 QY 180 CC-GGCCACCTTGGAGTCCCGGTTAGGCATGGGGACCTCTCCGAGCAGCAGCACCGC 238  
 DB 216 CCGGCGCGCGCTGCGAGTCCCGGTTAGGCATGGGGACCTCTCCGAGCAGCAGCACCGC 275  
 QY 239 CCTGCGCTCTGCGAGCGCATGCGCCGCGAGCCACAGCAGCAGCATGATCGCGGCTCCCT 298  
 DB 276 CCTGCGCTCTGCGAGCGCATGCGCCGCGAGCCACAGCAGCAGCATGATGCGCGGCTCCCT 335  
 QY 299 TCTCCTGCTTGGATTCTTACGACACACAGAGTTCAGCAGAGAGAGCGCTCGAATCT 358  
 DB 336 TCTCCTGCTTGGATTCTTACGACACACAGAGTTCAGCAGAGAGAGCGCTCGAATCT 395  
 QY 359 CATTGGCAGATACCGCCATGTTACCGTGCACCGCGCAGGTGTTAACTGTGACAGTG 418  
 DB 396 CATTGGCAGATACCGCCATGTTACCGTGCACCGCGCAGGTGTTAACTGTGACAGTG 455  
 QY 419 TCCAGCAGGAGCCTATGCTCTGAGCATTTCTACACAGAGCTGCGCTCTGACGAG 478  
 DB 456 TCCAGCAGGAGCCTATGCTCTGAGCATTTCTACACAGAGCTGCGCTCTGACGAG 515

QY 479 TTGCCCTGTGGGACCTTTTACAGGCAATGAGAAATGAGAAATGCACTGTAG 538  
 DB 516 TTGCCCTGTGGGACCTTTTACAGGCAATGAGAAATGAGAAATGCACTGTAG 575  
 QY 539 TCAGCCATGCCCATGCCCAATGATTGAGAAATTACCTTGTGCTGCC 584  
 DB 576 TCAGCCATGCCCATGCCCAATGATTGAGAAATTACCTTGTGCTGCC 621

RESULT 14  
 ADN95920  
 ID ADN95920 standard; DNA; 3662 BP.  
 XX  
 AC ADN95920;  
 XX  
 DT 01-JUL-2004 (first entry)  
 XX  
 DE Human BEC/LEC-related gene sequence SeqID844.  
 XX  
 KW growth; differentiation; blood endothelial cell; BEC;  
 KW lymphatic endothelial cell; LEC; hereditary lymphoedema; VEGFR-3;  
 KW lymphatic growth agent; VEGF-C; VEGF-D; antiangiogenic; cytoskeletal;  
 KW vasotropic; antiinflammatory; gene therapy; endothelial cell disorder;  
 KW inflammatory disease; cancer metastasis; lymphatic system; gene; ds;  
 KW human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003080640-A1.  
 XX  
 PD 02-OCT-2003.  
 XX  
 PF 07-MAR-2003; 2003WO-US0006900.  
 XX  
 PR 07-MAR-2002; 2002US-0363019P.  
 XX  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 PA (LICN ) LICENTIA LTD.  
 PI Alitalo K, Makinen T, Petrova T, Saharinen P, Saharinen J;  
 DR WPI; 2003-876899/81.  
 DR P-PSDB; ADN95919.  
 XX  
 PS Example 1; SEQ ID NO 844; 176pp; English.  
 CC This invention relates to a method of differentially modulating the  
 CC growth or differentiation of blood endothelial cells (BEC) or lymphatic  
 CC endothelial cells (LEC) comprising contacting endothelial cells with a  
 CC composition comprising an agent that differentially modulates blood or  
 CC lymphatic endothelial cells. Treating hereditary lymphoedema comprises  
 CC identifying a human subject with lymphoedema and with a mutation in at  
 CC least one allele of a gene encoding a LEC protein, where the mutation  
 CC correlates with lymphoedema in human subjects, and with the proviso that  
 CC the LEC protein is not VEGFR-3; and administering to the subject a  
 CC composition comprising a lymphatic growth agent selected from VEGF-C or  
 CC VEGF-D polypeptides and polynucleotides. The invention may be useful for  
 CC the development of compounds with an antiangiogenic, cytoskeletal,  
 CC vasotropic or antiinflammatory activity or for gene therapy. The method  
 CC is useful in modulating the growth or differentiation of blood  
 CC endothelial cells or lymphatic endothelial cells, in treating hereditary  
 CC lymphoedema, in screening for an endothelial cell disorder or  
 CC of a drug on endothelial cells. The agent is useful in manufacturing a  
 CC medicament for the differential modulation of blood vessel endothelial  
 CC cell or lymphatic vessel endothelial cell growth or differentiation. The  
 CC lymphatic growth agent may also be used in manufacturing a medicament for  
 CC the treatment of hereditary lymphoedema resulting from a mutation in a  
 CC LEC gene or of other diseases involving the lymphatic vessels, such as  
 CC various inflammatory diseases and cancer metastasis via the lymphatic  
 CC system. The present sequence is that of a human LEC/BEC differentially  
 CC expressed gene which is related to the method of the invention. Note: This  
 CC sequence does not appear in the specification but was obtained by the

CC indexer using the source data given in table 14 of the specification.

XX SQ Sequence 3662 BP; 864 A; 960 C; 899 G; 939 T; 0 U; 0 Other;  
Query Match 93.3%; Score 544.8; DB 11; Length 3662;  
Best Local Similarity 97.4%; Pred. No. 1.1e-117;  
Matches 571; Conservative 0; Mismatches 13; Indels 2; Gaps 2;  
QY 1 GCGGCCGCGGNGNGCAAGTGCTGAGCGCCCTAGNCCCTCCCTTGCCTCCCTCC 60  
Db 223 GCGGCCGCGCGCTGGCGAGTCTGAGCGCCCTAGAGCCTCTTGCCTCCCTCC 282  
QY 61 TCTGCCCGCGCTAGCAGTGCACATGGGGTGTGGAGGTAGATGGCTCCCGG-CGGGA 119  
Db 283 TCTGCCCGCGCGCAGCAGTGCACATGGGGTGTGGAGGTAGATGGCTCCCGCGCGGA 342  
QY 120 GCGCGCGGTGGATGCGCGCGTGGGCGAGAGCAGCCCGCATTCACGCTGCGCGCGGCC 179  
Db 343 GCGCGCGGTGGATGCGCGCGTGGGCGAGAGCAGCCCGCATTCACGCTGCGCGCGGCC 402  
QY 180 CC-GGCCACCTTGCAGTCCCGGTTCCAGCATGGGGAACCTTCCGAGCAGCAGCACCGC 238  
Db 403 CCGGCGCGCTTCCGAGTCCCGGTTCCAGCATGGGGAACCTTCCGAGCAGCAGCACCGC 462  
QY 239 CCTCGCTCTGCGAGCGCATGCGCGCGAGCCAGCCAGCAGCATGATCGCGGCTCCCT 298  
Db 463 CCTCGCTCTGCGAGCGCATGCGCGCGAGCCAGCCAGCAGCATGATCGCGGCTCCCT 522  
QY 299 TCTCTGCTTGGATTCTTAGCACCCAGCAGCTCAGCCAGCAAGAGGCTTCGAATCT 358  
Db 523 TCTCTGCTTGGATTCTTAGCACCCAGCAGCTCAGCCAGCAAGAGGCTTCGAATCT 582  
QY 359 CATTCGCACATACCGCATGTTGACCGTGCCACCGCGCAGGTCTAACCTGTGACAAAGT 418  
Db 583 CATTCGCACATACCGCATGTTGACCGTGCCACCGCGCAGGTCTAACCTGTGACAAAGT 642  
QY 419 TCCAGCAGGAACCTATGCTCTCAGCATTTACCAACAGCGCTGCGGTCTGCAGCAG 478  
Db 643 TCCAGCAGGAACCTATGCTCTCAGCATTTACCAACAGCGCTGCGGTCTGCAGCAG 702  
QY 479 TTGCTCTGTGGGACCTTTACAGGCGATGAGATGGCATAGAGAAATGCCATGACTGTAG 538  
Db 703 TTGCTCTGTGGGACCTTTACAGGCGATGAGATGGCATAGAGAAATGCCATGACTGTAG 762  
QY 539 TCAGCATGCGCATGCGCAATGATTGAGAAATTAACCTGTGCTGCC 584  
Db 763 TCAGCATGCGCATGCGCAATGATTGAGAAATTAACCTGTGCTGCC 808

RESULT 15

AAZ33945  
ID AAZ33945 standard; cDNA; 3534 BP.

XX AAZ33945;  
AC AAZ33945;

XX 07-DEC-1999 (first entry)  
DT 07-DEC-1999 (first entry)

XX Human PRO868 nucleotide sequence.  
DE Human PRO868 nucleotide sequence.

XX Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;  
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;  
KW secreted protein; transmembrane protein; ss.

XX Homo sapiens.  
XX

XX WO9946281-A2.  
PN

XX 16-SEP-1999.  
PD

XX 08-MAR-1999; 99WO-US005028.  
XX

XX 10-MAR-1998; 98US-0077450P.  
PR

XX 11-MAR-1998; 98US-0077632P.  
PR

PR 11-MAR-1998; 98US-0077641P.  
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PR 30-JUL-1998; 98US-0094651P.  
PR 11-SEP-1998; 98US-0100038P.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
XX  
XX  
PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;  
XX  
XX  
DR WPI; 1999-551358/46.  
DR P-PSDB; AAY41693.  
XX  
XX  
PT New secreted and transmembrane polypeptides and their polynucleotides,  
PT useful for treating blood coagulation disorders, cancers and cellular  
PT adhesion disorders.  
XX  
XX  
PS Claim 2; Fig 25; 530pp; English.  
XX  
XX

CC The present invention describes secreted and transmembrane polypeptides  
CC and their polynucleotides. The nucleotide sequences are useful as sources  
CC of probes, primers, for chromosome mapping, and for generation of  
CC antisense sequences. They can also be used to create transgenic animals.  
CC The proteins can be used to treat a variety of diseases and disorders,  
CC depending on their function. Diseases that may be treated include blood  
CC coagulation disorders, cancers and cellular adhesion disorders. They may  
CC also be used to raise antibodies. AA233891 to AA234338, and AA41685 to  
CC AA41774 represent polynucleotide and polypeptide sequence given in the  
CC exemplification of the present invention  
XX  
XX

SQ Sequence 3534 BP; 829 A; 927 C; 858 G; 920 T; 0 U; 0 Other;

Query Match 93.0%; Score 543.2; DB 2; Length 3534;  
Best Local Similarity 97.3%; Pred. No. 2.5e-117;  
Matches 570; Conservative 0; Mismatches 14; Indels 2; Gaps 2;  
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OM nucleic - nucleic search, using sw model

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Searched: 824507 seqs, 355394441 residues  
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Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2          | 578   | 99.0        | 584    | 4  | US-09-314-844F-3    |
| 3          | 550.2 | 94.2        | 588    | 4  | US-09-314-844F-5    |
| 4          | 544.8 | 93.3        | 2638   | 3  | US-09-042-785A-22   |
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Sequence 7, Appli  
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ALIGNMENTS

RESULT 1  
US-08-959-382-3  
; Sequence 3, Application US/08959382  
; Patent No. 6013476  
; GENERAL INFORMATION:  
; APPLICANT: DEEN, KEITH  
; APPLICANT: HURLE, MARK  
; APPLICANT: YOUNG, PETER  
; APPLICANT: TAN, K.B.  
; TITLE OF INVENTION: Tumor Necrosis Related Receptor,  
; TITLE OF INVENTION: TR7  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: RATNER & PRESTIA  
; STREET: P.O. BOX 980  
; CITY: VALLEY FORGE  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19482  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/959,382  
; FILING DATE: 28-OCT-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/041,796  
; FILING DATE: 02-APR-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PRESTIA, PAUL F  
; REGISTRATION NUMBER: 23,031  
; REFERENCE/DOCKET NUMBER: GH-50017  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-407-0700  
; TELEFAX: 610-407-0701  
; TELEX: 846169  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 584 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; US-08-959-382-3

Query Match 99.0%; Score 578; DB 3; Length 584;  
Best Local Similarity 100.0%; Pred. No. 1.8e-135;

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## RESULT 2

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; Sequence 3, Application US/09314844F
; Patent No. 6660839
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH CHARLES
; APPLICANT: HURLE, MARK R.
; APPLICANT: YOUNG, PETER
; APPLICANT: TAN, K. B.
; TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS RELATED
; FILE REFERENCE: GH-50017-1
; CURRENT APPLICATION NUMBER: US/09/314,844F
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 60/041,796
; PRIOR FILING DATE: 1997-04-02
; PRIOR APPLICATION NUMBER: US 08/959,382
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 584
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (4) (10) (11) (13) (15) (38)
; OTHER INFORMATION: OTHER INFORMATION: n= a, g, c or t
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Query Match 99.0%; Score 578; DB 4; Length 584;
Best Local Similarity 100.0%; Pred. No. 1.8e-115;
Matches 584; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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US-09-314-844F-5
; Sequence 5, Application US/09314844F
; Patent No. 6660839
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH CHARLES
; APPLICANT: HURLE, MARK R.
; APPLICANT: YOUNG, PETER
; APPLICANT: TAN, K. B.
; TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS RELATED
; FILE REFERENCE: GH-50017-1
; CURRENT APPLICATION NUMBER: US/09/314,844F
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 60/041,796
; PRIOR FILING DATE: 1997-04-02
; PRIOR APPLICATION NUMBER: US 08/959,382
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 588
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (4) (10) (11) (13) (15) (38)
; OTHER INFORMATION: OTHER INFORMATION: n= a, g, c or t
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US-09-314-844F-5

Query Match 94.2%; Score 550.2; DB 4; Length 588;  
Best Local Similarity 98.5%; Pred. No. 1.6e-128;  
Matches 572; Conservative 0; Mismatches 8; Indels 1; Gaps 1;  
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RESULT 4

US-09-042-785A-22  
; Sequence 22, Application US/09042785A  
; Patent No. 6194151  
; GENERAL INFORMATION:  
; APPLICANT: Busfield, Samantha J  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY  
; TITLE OF INVENTION: AND USES THEREFOR  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/042,785A  
; FILING DATE: 17-MAR-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/938,896

FILING DATE: 26-SEP-1997  
ATTORNEY/AGENT INFORMATION:  
; NAME: Mandragouras, Amy E  
; REGISTRATION NUMBER: 36,207  
; REFERENCE/DOCKET NUMBER: MEI-001CP  
TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)742-4214  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2638 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 510..2327  
US-09-042-785A-22

Query Match 93.3%; Score 544.8; DB 3; Length 2638;  
Best Local Similarity 97.4%; Pred. No. 5.4e-127;  
Matches 571; Conservative 0; Mismatches 13; Indels 2; Gaps 2;  
QY 1 GCGNCCGCGNNGNGCAAGGTCTGAGCGCCCTTAGNGCCTCCCTTGGCGCTCCCTCC 60  
DB 299 GCGGCGCGCGCTGGCGCAGGTGCTGAGCGCCCTTAGAGCCTCCCTTGGCGCTCCCTCC 358  
QY 61 TCTGCGCGCGGTAGCAGTGCACATGGGGTGTGGAGGTAGATGGCTCCCGG-CCGGGA 119  
DB 359 TCTGCGCGCGCGGTAGCAGTGCACATGGGGTGTGGAGGTAGATGGCTCCCGG-CCGGGA 418  
QY 120 GCGGCGCGGTGATGCGCGCTGGGCGAAGCAGCGCCCGCATTCACGCTGCCCCCGCGGCC 179  
DB 419 GCGGCGCGGTGATGCGCGCTGGGCGAAGCAGCGCCCGCATTCACGCTGCCCCCGCGGCC 478  
QY 180 CC-GGCGACCTTTCGAGTCCCCCGTTTACCGATGGGGACCTCTCCGAGCAGCAGCACCGC 238  
DB 479 CCGGCGCGCGCTTCGAGTCCCCCGTTTACCGATGGGGACCTCTCCGAGCAGCAGCACCGC 538  
QY 239 CCGGCGCGCGCTTCGAGTCCCCCGTTTACCGATGGGGACCTCTCCGAGCAGCAGCACCGC 298  
DB 539 CCGGCGCGCGCTTCGAGTCCCCCGTTTACCGATGGGGACCTCTCCGAGCAGCAGCACCGC 598  
QY 299 TCTCTGCTTGGATTCTTAGCACCACAGCTCAGCGCAGACAGAGGCTTCGAATCT 358  
DB 599 TCTCTGCTTGGATTCTTAGCACCACAGCTCAGCGCAGACAGAGGCTTCGAATCT 658  
QY 359 CATTGGCACAATACCGCCATGTTGACCGTGCACCGCGCCAGGTGCTAACCTGTGACAAGTG 418  
DB 659 CATTGGCACAATACCGCCATGTTGACCGTGCACCGCGCCAGGTGCTAACCTGTGACAAGTG 718  
QY 419 TCAGCAGGAACTTATGTTCTGAGCATTTGATACCAACAGCCTGGCGCTTCGAGCAG 478  
DB 719 TCAGCAGGAACTTATGTTCTGAGCATTTGATACCAACAGCCTGGCGCTTCGAGCAG 778  
QY 479 TTGCGCTGTGGGACCTTTTACAGGCATGAGAAATGCATAGAGAAATGCCATGACTGTAG 538  
DB 779 TTGCGCTGTGGGACCTTTTACAGGCATGAGAAATGCATAGAGAAATGCCATGACTGTAG 838  
QY 539 TCAGCCATGCCCATGGCCAAATGATTGAGAAATTAACCTTTGTGTGCC 584  
DB 839 TCAGCCATGCCCATGGCCAAATGATTGAGAAATTAACCTTTGTGTGCC 884

RESULT 5

US-09-527-236A-1  
; Sequence 1, Application US/09527236A  
; Patent No. 6358508  
; GENERAL INFORMATION:  
; APPLICANT: Ni, Jian  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Fan, Ping

APPLICANT: Gentz, Reiner L.  
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9  
FILE REFERENCE: PF375P1  
CURRENT APPLICATION NUMBER: US/09/527,236A  
CURRENT FILING DATE: 2000-03-16  
PRIOR APPLICATION NUMBER: 60/052,991  
PRIOR FILING DATE: 1997-06-11  
PRIOR APPLICATION NUMBER: 09/095,094  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/126,019  
PRIOR FILING DATE: 1999-03-24  
PRIOR APPLICATION NUMBER: 60/134,220  
PRIOR FILING DATE: 1999-05-14  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 3474  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (247)..(2211)  
NAME/KEY: sig\_peptide  
LOCATION: (247)..(366)  
NAME/KEY: mat\_peptide  
LOCATION: (367)..(2211)  
US-09-527-236A-1

Query Match 93.3%; Score 544.8; DB 3; Length 3474;  
Best Local Similarity 97.4%; Pred. No. 5.7e-127;  
Matches 571; Conservative 0; Mismatches 13; Indels 2; Gaps 2;  
QY 1 GCGNCCGCGNNGNGCAAGTGCTGAGCGCCCTAGNGCCTCCCTTGGCGGCTCCCTCC 60  
Db 36 GCGGCGCGCGCGTGGCAGGTGCTGAGCGCCCTTAGAGCCTCCCTTGGCGGCTCCCTCC 95  
QY 61 TCTGCCCGCGCGTAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCGG-CGGGA 119  
Db 96 TCTGCCCGCGCGCAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCGGCGCGG 155  
QY 120 GCGGCGGTGGATGCGGCGCTGGGCGAGCAGCGCGATTCAGGTGCGGCTCCCGGCGG 179  
Db 156 GCGGCGGTGGATGCGGCGCTGGGCGAGCAGCGCGGATTCAGGTGCGGCTCCCGGCGG 215  
QY 180 CC-GGCCACCTTCGAGTCCCGGTTTCAGCATGGGACCTCTCCGAGCAGCAGCAGC 238  
Db 216 CCGGGCGCCCTCGAGTCCCGGTTTCAGCATGGGACCTCTCCGAGCAGCAGCAGC 275  
QY 239 CTTGCGCTCTGTCAGCGCGCATGCGCGCGGAGCAGCAGCAGCAGTATGCGGGCTCCCT 298  
Db 276 CTTGCGCTCTGTCAGCGCGCATGCGCGCGGAGCAGCAGCAGCAGTATGCGGGCTCCCT 335  
QY 299 TCTCTGCTTGGATTCCTTAGCACACACACAGCTCAGCGCGAGCAGCAGCAGTATG 358  
Db 336 TCTCTGCTTGGATTCCTTAGCACACACACAGCTCAGCGCGAGCAGCAGCAGTATG 395  
QY 359 CATTGGCAGATCCGCGCATCTTCAGCGTGCCACCGCGCAGTGCTTAACCTGTGACAGTG 418  
Db 396 CATTGGCAGATCCGCGCATCTTCAGCGTGCCACCGCGCAGTGCTTAACCTGTGACAGTG 455  
QY 419 TCAGCAGGAACTATGTCTCTGAGCATTTGTACAAACAGCAGCTCGGCTCTGACAGCAG 478  
Db 456 TCAGCAGGAACTATGTCTCTGAGCATTTGTACAAACAGCAGCTCGGCTCTGACAGCAG 515  
QY 479 TTGCGCTTGGGACCTTTTACGAGCATGAGATGAGATGAGATGAGATGAGATGAGATG 538  
Db 516 TTGCGCTTGGGACCTTTTACGAGCATGAGATGAGATGAGATGAGATGAGATGAGATG 575  
QY 539 TCAGCATGCGCATGCGCATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 584  
Db 576 TCAGCATGCGCATGCGCATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 621

RESULT 6  
US-09-756-854-1  
Sequence 1, Application US/09756854  
Patent No. 6667390  
GENERAL INFORMATION:  
APPLICANT: Ni, Jian  
Yu, Guo-Liang  
Fan, Ping  
Gentz, Reiner  
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: MD  
COUNTRY: US  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/756,854  
FILING DATE: 10-Jan-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/095,094  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Hoover, Kenley K.  
REGISTRATION NUMBER: 40,302  
REFERENCE/DOCKET NUMBER: PF375  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8439  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3474 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 247..2211  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 367..2211  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 247..364  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-756-854-1

Query Match 93.3%; Score 544.8; DB 4; Length 3474;  
Best Local Similarity 97.4%; Pred. No. 5.7e-127;  
Matches 571; Conservative 0; Mismatches 13; Indels 2; Gaps 2;  
QY 1 GCGNCCGCGNNGNGCAAGTGCTGAGCGCCCTAGNGCCTCCCTTGGCGGCTCCCTCC 60  
Db 36 GCGGCGCGCGCGTGGCAGGTGCTGAGCGCCCTTAGAGCCTCCCTTGGCGGCTCCCTCC 95  
QY 61 TCTGCCCGCGCGTAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCGG-CGGGA 119  
Db 96 TCTGCCCGCGCGCAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCGGCGCGG 155  
QY 120 GCGGCGGTGGATGCGGCGCTGGGCGAGCAGCGCGATTCAGGTGCGGCTCCCGGCGG 179  
Db 156 GCGGCGGTGGATGCGGCGCTGGGCGAGCAGCGCGATTCAGGTGCGGCTCCCGGCGG 215  
QY 180 CC-GGCCACCTTTCGAGTCCCGGTTTCAGCATGGGACCTCTCCGAGCAGCAGCAGC 238

Db 216 CCGGGCCGCTCGAGTCCCGGTTCCAGCATGGGACCTCTCCGAGCAGCAGCCGC 275  
Qy 239 CCTCGCTCTCGAGCCGCTCGGCGCCGAGCCACAGCCAGCATGATCGGGCTCCCT 298  
Db 276 CCTCGCTCTCGAGCCGCTCGGCGCCGAGCCACAGCCAGCATGATCGGGCTCCCT 335  
Qy 299 TCTCCTCTGGATTCTCTAGCACCACACAGCTCAGCCAGAAAGGCTCGAATCT 358  
Db 336 TCTCCTCTGGATTCTCTAGCACCACACAGCTCAGCCAGAAAGGCTCGAATCT 395  
Qy 359 CATTTGGCAGCATACCGCATGTTGACCGTGCCACCGGCGAGTGCTAACCTGTGCAAGTG 418  
Db 396 CATTTGGCAGCATACCGCATGTTGACCGTGCCACCGGCGAGTGCTAACCTGTGCAAGTG 455  
Qy 419 TCAGCAGGAGCACTATGCTCTGAGCATTTGACCAACAGCTGCTGCGCTGTCAGCAG 478  
Db 456 TCAGCAGGAGCACTATGCTCTGAGCATTTGACCAACAGCTGCTGCGCTGTCAGCAG 515  
Qy 479 TTGCGCTGTGGGACCTTTTACAGGCGATGAGAAATGCGCATGACTGTAG 538  
Db 516 TTGCGCTGTGGGACCTTTTACAGGCGATGAGAAATGCGCATGACTGTAG 575  
Qy 539 TCAGCAGTGGCATGCGCATGATTTGAGAAATGCGCATGACTGTAG 584  
Db 576 TCAGCAGTGGCATGCGCATGATTTGAGAAATGCGCATGACTGTAG 621

RESULT 7

US-09-042-785A-3  
; Sequence 3, Application US/09042785A  
; Patent No. 6194151  
; GENERAL INFORMATION:  
; APPLICANT: Busfield, Samantha J  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY  
; TITLE OF INVENTION: AND USES THEREFOR  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/042,785A  
; FILING DATE: 17-MAR-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/938,896  
; FILING DATE: 26-SEP-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mandragoras, Amy E  
; REGISTRATION NUMBER: 36,207  
; REFERENCE/DOCKET NUMBER: MEI-001CP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)742-4214  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2612 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 190..951  
US-09-042-785A-3

Query Match 90.7%; Score 529.4; DB 3; Length 2612;  
Best Local Similarity 98.4%; Pred. No. 3.8e-123;  
Matches 555; Conservative 0; Mismatches 7; Indels 2; Gaps 2;  
Qy 23 GCTGAGGCGCCCTAGNGCCTTCCCTTGGCGGCTCTCCCTCTGCGCGCCGCTAGCAGTGCA 82  
Db 1 GCTCAGCGCCCTAGACCCCTTCCCTTGGCGGCTCTCCCTCTGCGCGCCGCTAGCAGTGCA 60  
Qy 83 CATGGGGGTGTTGAGGTAGATGGCTCCCGG-CGGGAGGCGGCGGTGGATGGGCGCTG 141  
Db 61 CATGGGGGTGTTGAGGTAGATGGCTCCCGGCGGAGCGGCGGTGGATGGGCGCTG 120  
Qy 142 GGCAGAGCAGCGCCGATTTCCAGCTGCCCGCGCGCCCC-GGCGACCTTTCGAGTCCCC 200  
Db 121 GGCAGAGCAGCGCCGATTTCCAGCTGCCCGCGCGCCCCGGGCGGCTTGGAGTCCCC 180  
Qy 201 GGTTCAGCCATGCGGACCTCTCCGAGCAGCAGCAGCGCTCTGCGCTCTGAGCGCATC 260  
Db 181 GGTTCAGCCATGCGGACCTCTCCGAGCAGCAGCAGCGCTCTGCGCTCTGAGCGCATC 240  
Qy 261 GCCCGCGGCGCCACAGCCAGCATGATGCGGGCTCCCTTCTCTGCTTGGATTCCTTAGC 320  
Db 241 GCCCGCGGCGCCACAGCCAGCATGATGCGGGCTCCCTTCTCTGCTTGGATTCCTTAGC 300  
Qy 321 ACCACACAGCTCAGCCAGAAAGAGGCTCGAATCTCATTTGGCAGCATACCGCATGTT 380  
Db 301 ACCACACAGCTCAGCCAGAAAGAGGCTCGAATCTCATTTGGCAGCATACCGCATGTT 360  
Qy 381 GACCGTGCCACCGGCGAGGTGCTAACTGTGCAAGTGTCCAGCAGAACTATGCTCT 440  
Db 361 GACCGTGCCACCGGCGAGGTGCTAACTGTGCAAGTGTCCAGCAGAACTATGCTCT 420  
Qy 441 GAGCATTTACCAACACAGCCCTGCGGCTGTGAGCAGATTTGCCCTGTGGGACCTTTACC 500  
Db 421 GAGCATTTACCAACACAGCCCTGCGGCTGTGAGCAGATTTGCCCTGTGGGACCTTTACC 480  
Qy 501 AGGCATGAGAAATGCGATAGAAATGCCATGCTGTAGTCAGCATGCCCATGCCCAATG 560  
Db 481 AGGCATGAGAAATGCGATAGAAATGCCATGCTGTAGTCAGCATGCCCATGCCCAATG 540  
Qy 561 ATTGAGAAATTTACCTTTGTGCTGCC 584  
Db 541 ATTGAGAAATTTACCTTTGTGCTGCC 564

RESULT 8

US-08-959-382-1  
; Sequence 1, Application US/08959382  
; Patent No. 6013476  
; GENERAL INFORMATION:  
; APPLICANT: DEEN, KEITH  
; APPLICANT: HURLE, MARK  
; APPLICANT: YOUNG, PETER  
; APPLICANT: TAN, K. B.  
; TITLE OF INVENTION: Tumor Necrosis Related Receptor,  
; TITLE OF INVENTION: TR7  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: RATNER & PRESTIA  
; STREET: P. O. BOX 980  
; CITY: VALLEY FORGE  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19482  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/959,382  
; FILING DATE: 28-OCT-1997

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; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/041,796
; FILING DATE: 02-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-50017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2186 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-959-382-1

Query Match          65.2%; Score 381; DB 3; Length 2186;
Best Local Similarity 100.0%; Pred. No. 4.4e-86;
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 TCAGCCATGGGACCTCTCCGAGCAGCAGCAGCGCCCTCGCTCCTCGAGCGCATCGCC 263
DB 1 TCAGCCATGGGACCTCTCCGAGCAGCAGCAGCGCCCTCGCTCCTCGAGCGCATCGCC 60
QY 264 CGCGGAGCCACAGCAGCATGATCGGGGCTCCCTTCTCTGCTGGATTCTTTAGCACC 323
DB 61 CGCGGAGCCACAGCAGCATGATCGGGGCTCCCTTCTCTGCTGGATTCTTTAGCACC 120
QY 324 ACCACAGCTCAGCCAGCAAGAGGCTCGAATCTCATTTGGCACATACCGCCATGTTGAC 383
DB 121 ACCACAGCTCAGCCAGCAAGAGGCTCGAATCTCATTTGGCACATACCGCCATGTTGAC 180
QY 384 CGTGCCACCGCCAGGTGCTAACTGTGACAAAGTGTCCAGCAGGAACCTATGTTCTGAG 443
DB 181 CGTGCCACCGCCAGGTGCTAACTGTGACAAAGTGTCCAGCAGGAACCTATGTTCTGAG 240
QY 444 CATTGTACCAACAAGCCTGCGGCTGTGACAGTTCGAGCAGTTGCCCTTGGGGACCTTTACCAG 503
DB 241 CATTGTACCAACAAGCCTGCGGCTGTGACAGTTCGAGCAGTTGCCCTTGGGGACCTTTACCAG 300
QY 504 CATGAGAATGGCATAGAAATGCCATGACTGTAGTCAGCCATGCCCATGGCCAAATGATT 563
DB 301 CATGAGAATGGCATAGAAATGCCATGACTGTAGTCAGCCATGCCCATGGCCAAATGATT 360
QY 564 GAGAAATTACCTTGTGCTGCC 584
DB 361 GAGAAATTACCTTGTGCTGCC 381

RESULT 9
US-09-314-844F-1
; Sequence 1, Application US/09314844F
; Patent No. 6660839
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH CHARLES
; APPLICANT: HURLE, MARK R.
; APPLICANT: YOUNG, PETER
; APPLICANT: TAN, K. B.
; TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS RELATED
; FILE REFERENCE: GH-50017-1
; CURRENT APPLICATION NUMBER: US/09/314,844F
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 60/041,796
; PRIOR FILING DATE: 1997-04-02
; PRIOR APPLICATION NUMBER: US 08/959,382
; PRIOR FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 6
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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2186
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
; US-09-314-844F-1

Query Match          65.2%; Score 381; DB 4; Length 2186;
Best Local Similarity 100.0%; Pred. No. 4.4e-86;
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 TCAGCCATGGGACCTCTCCGAGCAGCAGCAGCGCCCTCGCTCCTCGAGCGCATCGCC 263
DB 1 TCAGCCATGGGACCTCTCCGAGCAGCAGCAGCGCCCTCGCTCCTCGAGCGCATCGCC 60
QY 264 CGCGGAGCCACAGCAGCATGATCGGGGCTCCCTTCTCTGCTGGATTCTTTAGCACC 323
DB 61 CGCGGAGCCACAGCAGCATGATCGGGGCTCCCTTCTCTGCTGGATTCTTTAGCACC 120
QY 324 ACCACAGCTCAGCCAGCAAGAGGCTCGAATCTCATTTGGCACATACCGCCATGTTGAC 383
DB 121 ACCACAGCTCAGCCAGCAAGAGGCTCGAATCTCATTTGGCACATACCGCCATGTTGAC 180
QY 384 CGTGCCACCGCCAGGTGCTAACTGTGACAAAGTGTCCAGCAGGAACCTATGTTCTGAG 443
DB 181 CGTGCCACCGCCAGGTGCTAACTGTGACAAAGTGTCCAGCAGGAACCTATGTTCTGAG 240
QY 444 CATTGTACCAACAAGCCTGCGGCTGTGACAGTTCGAGCAGTTGCCCTTGGGGACCTTTACCAG 503
DB 241 CATTGTACCAACAAGCCTGCGGCTGTGACAGTTCGAGCAGTTGCCCTTGGGGACCTTTACCAG 300
QY 504 CATGAGAATGGCATAGAAATGCCATGACTGTAGTCAGCCATGCCCATGGCCAAATGATT 563
DB 301 CATGAGAATGGCATAGAAATGCCATGACTGTAGTCAGCCATGCCCATGGCCAAATGATT 360
QY 564 GAGAAATTACCTTGTGCTGCC 584
DB 361 GAGAAATTACCTTGTGCTGCC 381

RESULT 10
US-09-042-785A-6
; Sequence 6, Application US/09042785A
; Patent No. 6194151
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J
; TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,785A
; FILING DATE: 17-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/938,896
; FILING DATE: 26-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MEI-001CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
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TELEFAX: (617)742-4214  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 759 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..759  
US-09-042-785A-6

Query Match 64.2%; Score 375; DB 3; Length 759;  
Best Local Similarity 100.0%; Pred. No. 1.1e-84;  
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 210 ATGGGGACCTCTCGAGCAGCAGCAGCGCCCTCGCTTCTCTGCTTGGATTCCCTTAGCACCACCA 269
Db 1 ATGGGGACCTCTCGAGCAGCAGCAGCGCCCTCGCTTCTCTGCTTGGATTCCCTTAGCACCACCA 60
QY 270 GCCACAGCCACGATGATCGGGGCTCCCTTCTCTGCTTGGATTCCCTTAGCACCACCA 329
Db 61 GCCACAGCCACGATGATCGGGGCTCCCTTCTCTGCTTGGATTCCCTTAGCACCACCA 120
QY 330 GCTCAGCCAGAGGAGGCTCGAATCTCATTTGGCACAATACCGCCATGTTGACCGTGCC 389
Db 121 GCTCAGCCAGAGGAGGCTCGAATCTCATTTGGCACAATACCGCCATGTTGACCGTGCC 180
QY 390 ACCGGCAGGTGTAACCTGTGCAAGTGTCCAGCAGGAACCTATGTTCTGAGCATTTGT 449
Db 181 ACCGGCAGGTGTAACCTGTGCAAGTGTCCAGCAGGAACCTATGTTCTGAGCATTTGT 240
QY 450 ACCAACACAGCTGCGCGCTCGAGCAGTTCGCTTGGGGACCTTTACCGGCATGAG 509
Db 241 ACCAACACAGCTGCGCGCTCGAGCAGTTCGCTTGGGGACCTTTACCGGCATGAG 300
QY 510 AATGGCATAGAGAAATGCCATGACTGTAGTCAGCCATGCCCATGATTTAGAGAAA 569
Db 301 AATGGCATAGAGAAATGCCATGACTGTAGTCAGCCATGCCCATGATTTAGAGAAA 360
QY 570 TTACCTTGCTGCC 584
Db 361 TTACCTTGCTGCC 375
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## RESULT 11

US-09-042-785A-24  
; Sequence 24, Application US/09042785A  
; Patent No. 6194151  
; GENERAL INFORMATION:

APPLICANT: Busfield, Samantha J  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/042,785A  
; FILING DATE: 17-MAR-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/938,896  
; FILING DATE: 26-SEP-1997

ATTORNEY/AGENT INFORMATION:  
; NAME: Mandragouras, Amy E  
; REGISTRATION NUMBER: 36,207  
; REFERENCE/DOCKET NUMBER: MEI-001CP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)742-4214  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1815 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1815  
US-09-042-785A-24

Query Match 64.2%; Score 375; DB 3; Length 1815;  
Best Local Similarity 100.0%; Pred. No. 1.3e-84;  
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 210 ATGGGACCTCTCGAGCAGCAGCAGCGCCCTCGCTTCTCTGCTTGGATTCCCTTAGCACCACCA 269
Db 1 ATGGGACCTCTCGAGCAGCAGCAGCGCCCTCGCTTCTCTGCTTGGATTCCCTTAGCACCACCA 60
QY 270 GCCACAGCCACGATGATCGGGGCTCCCTTCTCTGCTTGGATTCCCTTAGCACCACCA 329
Db 61 GCCACAGCCACGATGATCGGGGCTCCCTTCTCTGCTTGGATTCCCTTAGCACCACCA 120
QY 330 GCTCAGCCAGAGGAGGCTCGAATCTCATTTGGCACAATACCGCCATGTTGACCGTGCC 389
Db 121 GCTCAGCCAGAGGAGGCTCGAATCTCATTTGGCACAATACCGCCATGTTGACCGTGCC 180
QY 390 ACCGGCAGGTGTAACCTGTGCAAGTGTCCAGCAGGAACCTATGTTCTGAGCATTTGT 449
Db 181 ACCGGCAGGTGTAACCTGTGCAAGTGTCCAGCAGGAACCTATGTTCTGAGCATTTGT 240
QY 450 ACCAACACAGCTGCGCGCTCGAGCAGTTCGCTTGGGGACCTTTACCGGCATGAG 509
Db 241 ACCAACACAGCTGCGCGCTCGAGCAGTTCGCTTGGGGACCTTTACCGGCATGAG 300
QY 510 AATGGCATAGAGAAATGCCATGACTGTAGTCAGCCATGCCCATGATTTAGAGAAA 569
Db 301 AATGGCATAGAGAAATGCCATGACTGTAGTCAGCCATGCCCATGATTTAGAGAAA 360
QY 570 TTACCTTGCTGCC 584
Db 361 TTACCTTGCTGCC 375
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## RESULT 12

US-09-527-236A-8/c  
; Sequence 8, Application US/09527236A  
; Patent No. 6358508  
; GENERAL INFORMATION:

APPLICANT: Ni, Jian  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Fan, Ping  
; APPLICANT: Gentz, Reiner L.  
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9  
; FILE REFERENCE: PF375P1  
; CURRENT APPLICATION NUMBER: US/09/527,236A  
; CURRENT FILING DATE: 2000-03-16  
; PRIOR APPLICATION NUMBER: 60/052,991  
; PRIOR FILING DATE: 1997-06-11  
; PRIOR APPLICATION NUMBER: 09/095,094  
; PRIOR FILING DATE: 1998-06-10  
; PRIOR APPLICATION NUMBER: 60/126,019  
; PRIOR FILING DATE: 1999-03-24  
; PRIOR APPLICATION NUMBER: 60/134,220  
; PRIOR FILING DATE: 1999-05-14

; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 345  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-527-236A-8

Query Match 45.1%; Score 263.6; DB 3; Length 345;  
Best Local Similarity 93.3%; Pred. No. 6e-57;  
Matches 319; Conservative 0; Mismatches 19; Indels 4; Gaps 4;  
QY 239 CTTGCTGCTGAGCGGATCGCCGCGAGCCAGCCAGCATGCGGGCTCCCT 298  
DB 345 CTTGCTGCTGAGCGGATCGCCGCGAGCCAGCCAGCATGCGGGCTCCCT 288  
QY 299 TCTCTGCTGCTGAGCGGATCGCCGCGAGCCAGCCAGCATGCGGGCTCCCT 358  
DB 287 TCTCTGCTGCTGAGCGGATCGCCGCGAGCCAGCCAGCATGCGGGCTCCCT 229  
QY 359 CATTGCGACATACCGGATCGCCGCGAGCCAGCCAGCATGCGGGCTCCCT 418  
DB 228 CATTGCGACATACCGGATCGCCGCGAGCCAGCCAGCATGCGGGCTCCCT 169  
QY 419 TCAGCAGGAGCACTATGCTCTGAGCATGCTACCAACACAGCGCTGCGGCTGCGAGCAG 478  
DB 168 TCAGCAGGAGCACTATGCTCTGAGCATGCTACCAACACAGCGCTGCGGCTGCGAGCAG 110  
QY 479 TTGCGCTGTGGGACCTTTACCAAGGATGAGATGCGATAGAGAAATGCGATGCTAG 538  
DB 109 TTGCGCTGTGGGACCTTTACCAAGGATGAGATGCGATAGAGAAATGCGATGCTAG 50  
QY 539 TCAGCAGGAGCACTATGCTCTGAGCATGCTACCAACACAGCGCTGCGGCTGCGAGCAG 580  
DB 49 TCAGCAGGAGCACTATGCTCTGAGCATGCTACCAACACAGCGCTGCGGCTGCGAGCAG 8

## RESULT 13

US-09-756-854-8/C

; Sequence 8, Application US/09756854

; Patent No. 6667390

; GENERAL INFORMATION:

; APPLICANT: Ni, Jian

; Pan, Ping

; Gentz, Reiner

; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: MD

; COUNTRY: US

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09756,854

; FILING DATE: 10-Jan-2001

; CLASSIFICATION: &lt;Unknown&gt;

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/095,094

; FILING DATE: &lt;Unknown&gt;

; ATTORNEY/AGENT INFORMATION:

; NAME: Hoover, Kenley K.

; REGISTRATION NUMBER: 40,302

; REFERENCE/DOCKET NUMBER: PF375

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 301-309-8504

; TELEFAX: 301-309-8439  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 345 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
US-09-756-854-8

Query Match 45.1%; Score 263.6; DB 4; Length 345;  
Best Local Similarity 93.3%; Pred. No. 6e-57;  
Matches 319; Conservative 0; Mismatches 19; Indels 4; Gaps 4;  
QY 239 CTTGCTGCTGAGCGGATCGCCGCGAGCCAGCCAGCATGCGGGCTCCCT 298  
DB 345 CTTGCTGCTGAGCGGATCGCCGCGAGCCAGCCAGCATGCGGGCTCCCT 288  
QY 299 TCTCTGCTGCTGAGCGGATCGCCGCGAGCCAGCCAGCATGCGGGCTCCCT 358  
DB 287 TCTCTGCTGCTGAGCGGATCGCCGCGAGCCAGCCAGCATGCGGGCTCCCT 229  
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QY 419 TCAGCAGGAGCACTATGCTCTGAGCATGCTACCAACACAGCGCTGCGGCTGCGAGCAG 478  
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DB 109 TTGCGCTGTGGGACCTTTACCAAGGATGAGATGCGATAGAGAAATGCGATGCTAG 50  
QY 539 TCAGCAGGAGCACTATGCTCTGAGCATGCTACCAACACAGCGCTGCGGCTGCGAGCAG 580  
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## RESULT 14

US-09-042-785A-1

; Sequence 1, Application US/09042785A

; Patent No. 6194151

; GENERAL INFORMATION:

; APPLICANT: Busfield, Samantha J

; TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE &amp; COCKFIELD, LLP

; STREET: 28 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/042,785A

; FILING DATE: 17-MAR-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/938,896

; FILING DATE: 26-SEP-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Mandragouras, Amy E

; REGISTRATION NUMBER: 36,207

; REFERENCE/DOCKET NUMBER: MEI-001CP

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617)227-7400



**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 8, 2005, 02:56:22 ; Search time 571 Seconds  
(without alignments)

5868.441 Million cell updates/sec

Title: US-10-663-157-3

Perfect score: 584

Sequence: 1 ggcncgcgmgngmgcaag.....agaattacctgtgtgtgcc 584

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4293498 seqs, 2868903791 residues

Total number of hits satisfying chosen parameters: 8586996

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

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- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
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- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
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- 18: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 19: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*
- 20: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 21: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description       |
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| 2          | 550.2 | 94.2        | 588    | 17 | US-10-663-157-5   |
| 3          | 544.8 | 93.3        | 2877   | 9  | US-09-840-795-5   |
| 4          | 544.8 | 93.3        | 3474   | 9  | US-09-756-854-1   |
| 5          | 544.8 | 93.3        | 3474   | 13 | US-10-041-574-1   |
| 6          | 544.8 | 93.3        | 3474   | 18 | US-10-834-966-1   |
| 7          | 543.2 | 93.0        | 3534   | 9  | US-09-788-295A-63 |
| 8          | 543.2 | 93.0        | 3534   | 9  | US-09-778-697-63  |
| 9          | 543.2 | 93.0        | 3534   | 9  | US-09-978-192A-63 |
| 10         | 543.2 | 93.0        | 3534   | 9  | US-09-999-832A-63 |
| 11         | 543.2 | 93.0        | 3534   | 10 | US-09-978-189-63  |
| 12         | 543.2 | 93.0        | 3534   | 10 | US-09-978-608A-63 |

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|----|-------|------|------|----|-------------------|
| 13 | 543.2 | 93.0 | 3534 | 10 | US-09-978-585A-63 |
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| 18 | 543.2 | 93.0 | 3534 | 10 | US-09-981-915A-63 |
| 19 | 543.2 | 93.0 | 3534 | 10 | US-09-978-824-63  |
| 20 | 543.2 | 93.0 | 3534 | 10 | US-09-918-585A-63 |
| 21 | 543.2 | 93.0 | 3534 | 10 | US-09-999-834A-63 |
| 22 | 543.2 | 93.0 | 3534 | 10 | US-09-978-423A-63 |
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| 24 | 543.2 | 93.0 | 3534 | 10 | US-09-999-830A-63 |
| 25 | 543.2 | 93.0 | 3534 | 10 | US-09-978-757A-63 |
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| 27 | 543.2 | 93.0 | 3534 | 10 | US-09-978-643A-63 |
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| 30 | 543.2 | 93.0 | 3534 | 10 | US-09-978-188A-63 |
| 31 | 543.2 | 93.0 | 3534 | 10 | US-09-978-681A-63 |
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| 33 | 543.2 | 93.0 | 3534 | 10 | US-09-999-829A-63 |
| 34 | 543.2 | 93.0 | 3534 | 10 | US-09-978-299A-63 |
| 35 | 543.2 | 93.0 | 3534 | 10 | US-09-978-544A-63 |
| 36 | 543.2 | 93.0 | 3534 | 10 | US-09-978-865A-63 |
| 37 | 543.2 | 93.0 | 3534 | 10 | US-09-978-802A-63 |
| 38 | 543.2 | 93.0 | 3534 | 11 | US-09-999-831A-63 |
| 39 | 543.2 | 93.0 | 3534 | 13 | US-10-052-586-417 |
| 40 | 543.2 | 93.0 | 3534 | 14 | US-10-174-590-417 |
| 41 | 543.2 | 93.0 | 3534 | 14 | US-10-176-758-417 |
| 42 | 543.2 | 93.0 | 3534 | 14 | US-10-175-737-417 |
| 43 | 543.2 | 93.0 | 3534 | 14 | US-10-174-581-417 |
| 44 | 543.2 | 93.0 | 3534 | 14 | US-10-176-483-417 |
| 45 | 543.2 | 93.0 | 3534 | 14 | US-10-176-749-417 |

ALIGNMENTS

RESULT 1

US-10-663-157-3  
; Sequence 3, Application US/10663157  
; Publication No. US20040132057A1  
; GENERAL INFORMATION:  
; APPLICANT: DEEN, KEITH CHARLES  
; APPLICANT: HURLE, MARK R.  
; APPLICANT: YOUNG, PETER  
; APPLICANT: TAN, K.B.  
; TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS RELATED RECEPTOR TR7  
; FILE REFERENCE: SKBG-3017US2  
; CURRENT APPLICATION NUMBER: US/10/663,157  
; CURRENT FILING DATE: 2003-09-15  
; PRIOR APPLICATION NUMBER: US 60/041,796  
; PRIOR FILING DATE: 1997-04-02  
; PRIOR APPLICATION NUMBER: US 08/959,382  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: US 09/314,844  
; PRIOR FILING DATE: 1999-05-19  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3  
; LENGTH: 584  
; TYPE: DNA  
; ORGANISM: HOMO SAPIENS  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (4)..(4)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (10)..(11)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc\_feature

LOCATION: (13)...(13)  
OTHER INFORMATION: n is a, c, g, or t  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (15)...(15)  
OTHER INFORMATION: n is a, c, g, or t  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (38)...(38)  
OTHER INFORMATION: n is a, c, g, or t  
US-10-663-157-3

Query Match 99.0%; Score 578; DB 17; Length 584;  
Best Local Similarity 100.0%; Pred. No. 5e-154;  
Matches 584; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCGNCGCGNNGNGCAAGTGTGAGCGCCCTAGNGCCTCCCTTGGCGCTCCCTCC 60  
Db 1 GCGNCGCGNNGNGCAAGTGTGAGCGCCCTAGNGCCTCCCTTGGCGCTCCCTCC 60  
QY 61 TCTGCCCGCGGTAGCAGTGCATGCGGTGTGGAGGTAGATGGCTCCCGCGCGGAG 120  
Db 61 TCTGCCCGCGGTAGCAGTGCATGCGGTGTGGAGGTAGATGGCTCCCGCGCGGAG 120  
QY 121 GCGCGGTGTGATGCGCGCTGGCGCAGAGCAGCGCGCGATTCAGCTGCGCGCGCC 180  
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QY 181 CGGCCACCTTGCAGTCCCGGTTCAGCCATGCGGACCTTCAGAGCAGCAGCGCC 240  
Db 181 CGGCCACCTTGCAGTCCCGGTTCAGCCATGCGGACCTTCAGAGCAGCAGCGCC 240  
QY 241 TGCCCTCTCGACGCGCATCGCCCGCGAGCCAGCCAGATGATGCGGGGTCCCTTC 300  
Db 241 TGCCCTCTCGACGCGCATCGCCCGCGAGCCAGCCAGATGATGCGGGGTCCCTTC 300  
QY 301 TCCTGTGTGATTCCTTAGCACCAACACAGCTCAGCCAGAACAGAGGCTCGAATCTCA 360  
Db 301 TCCTGTGTGATTCCTTAGCACCAACACAGCTCAGCCAGAACAGAGGCTCGAATCTCA 360  
QY 361 TTGGCACAATACCGCATGTTGACCGTCCACCGCGCAGGTGCTAACTGTGACAAAGTTC 420  
Db 361 TTGGCACAATACCGCATGTTGACCGTCCACCGCGCAGGTGCTAACTGTGACAAAGTTC 420  
QY 421 CAGCAGAACCTATGCTCTGAGCATTTACCAACACAGCTGCGCGTCTGAGCAGTT 480  
Db 421 CAGCAGAACCTATGCTCTGAGCATTTACCAACACAGCTGCGCGTCTGAGCAGTT 480  
QY 481 GCCTGTGGGACCTTTACAGGCATGAGAAATGGCATAGAAATGCCATGACTGTAGTC 540  
Db 481 GCCTGTGGGACCTTTACAGGCATGAGAAATGGCATAGAAATGCCATGACTGTAGTC 540  
QY 541 AGCCATGCCATGGCAATGATTGAGAAATTAATCTTGTGTGCC 584  
Db 541 AGCCATGCCATGGCAATGATTGAGAAATTAATCTTGTGTGCC 584

## RESULT 2

US-10-663-157-5  
Sequence 5, Application US/10663157  
Publication No. US20040132057A1  
GENERAL INFORMATION:  
APPLICANT: DEEN, KEITH CHARLES  
APPLICANT: HURLE, MARK R.  
APPLICANT: YOUNG, PETER  
APPLICANT: TAN, K.B.  
TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS RELATED RECEPTOR TR7  
FILE REFERENCE: SKBG-3017US2  
CURRENT APPLICATION NUMBER: US/10/663,157  
CURRENT FILING DATE: 2003-09-15  
PRIOR APPLICATION NUMBER: US 60/041,796  
PRIOR FILING DATE: 1997-04-02  
PRIOR APPLICATION NUMBER: US 08/959,382

PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: US 09/314,844  
PRIOR FILING DATE: 1999-05-19  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 5  
LENGTH: 588  
TYPE: DNA  
ORGANISM: HOMO SAPIENS  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (4)...(4)  
OTHER INFORMATION: n is a, c, g, or t  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (10)...(11)  
OTHER INFORMATION: n is a, c, g, or t  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (13)...(13)  
OTHER INFORMATION: n is a, c, g, or t  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (15)...(15)  
OTHER INFORMATION: n is a, c, g, or t  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (38)...(38)  
OTHER INFORMATION: n is a, c, g, or t  
US-10-663-157-5

Query Match 94.2%; Score 550.2; DB 17; Length 588;  
Best Local Similarity 98.5%; Pred. No. 3.9e-146;  
Matches 572; Conservative 0; Mismatches 8; Indels 1; Gaps 1;  
QY 1 GCGNCGCGNNGNGCAAGTGTGAGCGCCCTAGNGCCTCCCTTGGCGCTCCCTCC 60  
Db 1 GCGNCGCGNNGNGCAAGTGTGAGCGCCCTAGNGCCTCCCTTGGCGCTCCCTCC 60  
QY 61 TCTGCCCGCGGTAGCAGTGCATGCGGTGTGGAGGTAGATGGCTCCCGCGCGGAG 120  
Db 61 TCTGCCCGCGGTAGCAGTGCATGCGGTGTGGAGGTAGATGGCTCCCGCGCGGAG 120  
QY 121 GCGCGGTGTGATGCGCGCTGGCGCAGAGCAGCGCGATTCAGCTGCGCGCGCC 180  
Db 121 GCGCGGTGTGATGCGCGCTGGCGCAGAGCAGCGCGATTCAGCTGCGCGCGCC 180  
QY 181 CGGCCACCTTGCAGTTCCTTGGAGTCCCGTTGAGCCATGGGACCTTCCTCGAGCAGCAGCGCC 240  
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QY 300 CTCCTGTGTGATTCCTTAGCACCACAGCTCAGCCAGAACAGAGGCTTCGAATCTC 359  
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Db 421 CCAGCAGGAACCTATGCTCTGAGCATTTGACCAACACAGCTGCGGTCTGCAGCAT 480  
QY 480 TCCTCTGTGGGACCTTTACAGGATGAGAAATGGCATAGAAATGCCATGACTGTAGT 539  
Db 481 TCCTCTGTGGGACCTTTACAGGATGAGAAATGGCATAGAAATGCCATGACTGTAGT 540  
QY 540 CAGCCATGCCATGGCCCAATGATTGAGAAATTAATCTTGTGCC 580  
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Db 541 CAGCCATGCCATGGCCCAATGATTGAGAAATTACCTTGTGTC 581

## RESULT 3

US-09-840-795-5  
; Sequence 5, Application US/09840795  
; Patent No. US20020143147A1  
; GENERAL INFORMATION:  
; APPLICANT: Murphy, Erin E.  
; APPLICANT: Mattson, Jeanine D.  
; APPLICANT: Bates, Elizabeth Esther Mary  
; APPLICANT: Gorman, Daniel M.  
; APPLICANT: Lebecque, Serge J.E.  
; TITLE OF INVENTION: Mammalian Genes; Related Reagents  
; FILE REFERENCE: SF0818K  
; CURRENT APPLICATION NUMBER: US/09/840,795  
; CURRENT FILING DATE: 2001-04-23  
; PRIOR APPLICATION NUMBER: 09/351,777  
; PRIOR FILING DATE: 1999-07-12  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 2877  
; TYPE: DNA  
; ORGANISM: primate  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (410)..(2374)  
; NAME/KEY: mat\_peptide  
; LOCATION: (533)..(2374)  
US-09-840-795-5

Query Match 93.3%; Score 544.8; DB 9; Length 2877;  
Best Local Similarity 97.4%; Pred. No. 1.5e-144;  
Matches 571; Conservative 0; Mismatches 13; Indels 2; Gaps 2;  
QY 1 GCGNCGCGNNGNGNGCAAGGTCTGAGCGCCCTAGNGCTCCCTTGGCGCTCCCTCC 60  
Db 199 GCGCGCGCGCGGTGGGCGAGTGTGAGCGCCCTAGCGCTCCCTTGGCGCTCCCTCC 258  
QY 61 TCTGCCCGCGGTAGCAGTGCATGGGGTGTGGAGGTAGATGGGTCCCGG-CCGGGA 119  
Db 259 TCTGCCCGCGCGAGCAGTGCATGGGGTGTGGAGGTAGATGGGTCCCGGCGCGGGA 318  
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Db 319 GCGCGCGGTGGATGCGCGGTGGGCAAGCAGCGCGCGGTTCAGCTGCGCGCGCGCC 378  
QY 180 CC-GGCCACCTTGGAGTTCCTTGGAGTTCCTTGGAGTTCCTTGGAGTTCCTTGGAGTTC 238  
Db 379 CCGCGCGCGCTGCGAGTTCCTTGGAGTTCCTTGGAGTTCCTTGGAGTTCCTTGGAGTTC 438  
QY 239 CTTGCGCTCTGCGAGCGCGATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 298  
Db 439 CTTGCGCTCTGCGAGCGCGATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 498  
QY 299 TCTCTCTCTTGGATTCTTGGAGTTCCTTGGAGTTCCTTGGAGTTCCTTGGAGTTCCT 358  
Db 499 TCTCTCTCTTGGATTCTTGGAGTTCCTTGGAGTTCCTTGGAGTTCCTTGGAGTTCCT 558  
QY 359 CATTTGGCACATACCGCATGTTGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 418  
Db 559 CATTTGGCACATACCGCATGTTGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 618  
QY 419 TCCAGCAGGAACTATGTTCTTGGAGTTCCTTGGAGTTCCTTGGAGTTCCTTGGAGTTC 478  
Db 619 TCCAGCAGGAACTATGTTCTTGGAGTTCCTTGGAGTTCCTTGGAGTTCCTTGGAGTTC 678  
QY 479 TTGCGCTCTGCGGACCTTTTACCAGGCGATGAGATGGCATGAGAAATGCCACTGCTAG 538  
Db 679 TTGCGCTCTGCGGACCTTTTACCAGGCGATGAGATGGCATGAGAAATGCCACTGCTAG 738  
QY 539 TCAGCCATGCCCATGGCCCAATGATTGAGAAATTACCTTGTGCTGCC 584

Db 739 TCAGCCATGCCCATGGCCCAATGATTGAGAAATTACCTTGTGCTGCC 784

## RESULT 4

US-09-756-854-1  
; Sequence 1, Application US/09756854  
; Patent No. US20020164684A1  
; GENERAL INFORMATION:  
; APPLICANT: Ni, Jian  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Fan, Ping  
; APPLICANT: Gentz, Reiner  
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: MD  
; COUNTRY: US  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/756,854  
; FILING DATE: 10-Jan-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/095,094  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hoover, Kenley K.  
; REGISTRATION NUMBER: 40,302  
; REFERENCE/DOCKET NUMBER: PF375  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 301-309-8504  
; TELEFAX: 301-309-8439  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3474 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 247..2211  
; FEATURE:  
; NAME/KEY: mat\_peptide  
; LOCATION: 367..2211  
; FEATURE:  
; NAME/KEY: sig\_peptide  
; LOCATION: 247..364  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-756-854-1

Query Match 93.3%; Score 544.8; DB 9; Length 3474;  
Best Local Similarity 97.4%; Pred. No. 1.6e-144;  
Matches 571; Conservative 0; Mismatches 13; Indels 2; Gaps 2;  
QY 1 GCGNCGCGNNGNGNGCAAGGTCTGAGCGCCCTAGNGCTCCCTTGGCGCTCCCTCC 60  
Db 36 GCGCGCGCGCGCGTGGGCGAGTGTGAGCGCCCTAGAGCTCCCTTGGCGCTCCCTCC 95  
QY 61 TCTGCCCGCGCGGTAGCAGTGCACATGGGTGTGGAGGTAGATGGGTCCCGG-CCGGGA 119  
Db 96 TCTGCCCGCGCGCGAGCAGTGCACATGGGTGTGGAGGTAGATGGGTCCCGGCGCGGA 155  
QY 120 GCGCGCGGTGGATGCGCGCGTGGGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 179

Db 156 GCGGCGGCTGGATGCGGCGCTGGGCAAGCAGCGCCGATTCAGCTGCCCGCGGCC 215  
Qy 180 CC-GGCACCTTGGAGTCCCGGTTGAGCATGGGGACCTCTCCGAGCAGCAGCAGCCG 238  
Db 216 CCGGGCGCCCTTGGAGTCCCGGTTGAGCATGGGGACCTCTCCGAGCAGCAGCAGCCG 275  
Qy 239 CTTGCGCTCTGACGCGCGCATGCGCGCGGAGCAGCAGCAGCAGCAGCAGCAGCAGC 298  
Db 276 CTTGCGCTCTGACGCGCGCATGCGCGCGGAGCAGCAGCAGCAGCAGCAGCAGCAGC 335  
Qy 299 TCTCTGCTTGGATTCTTACGACCCACACAGCTCAGCCAGAACAGAGGCTTCGAATCT 358  
Db 336 TCTCTGCTTGGATTCTTACGACCCACACAGCTCAGCCAGAACAGAGGCTTCGAATCT 395  
Qy 359 CATTGGCAGATACCGGCATTTGACCGTGCACCGCGCAGGTGTAACCTGTGACAAGTG 418  
Db 396 CATTGGCAGATACCGGCATTTGACCGTGCACCGCGCAGGTGTAACCTGTGACAAGTG 455  
Qy 419 TCCAGCAGGAACCTATGCTCTGAGCATTTGACCATGAGATGGCATAGAGAAATGCCATGCTGTAG 478  
Db 456 TCCAGCAGGAACCTATGCTCTGAGCATTTGACCATGAGATGGCATAGAGAAATGCCATGCTGTAG 515  
Qy 479 TTGCGCTGTGGGACCTTTACAGGCGATGAGATGGCATAGAGAAATGCCATGCTGTAG 538  
Db 516 TTGCGCTGTGGGACCTTTACAGGCGATGAGATGGCATAGAGAAATGCCATGCTGTAG 575  
Qy 539 TCAGCCATGCCCATGCCCAATGATTGAGAAATACCTTTGTGTGCC 584  
Db 576 TCAGCCATGCCCATGCCCAATGATTGAGAAATACCTTTGTGTGCC 621

## RESULT 5

US-10-041-574-1  
; Sequence 1, Application US/10041574  
; Publication No. US20020168359A1  
; GENERAL INFORMATION:  
; APPLICANT: Ni, Jian  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Fan, Ping  
; APPLICANT: Gentz, Reiner L.  
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9  
; FILE REFERENCE: PF375P1  
; CURRENT APPLICATION NUMBER: US/10/041,574  
; CURRENT FILING DATE: 2002-01-10  
; PRIOR APPLICATION NUMBER: 09/527,236  
; PRIOR FILING DATE: 2000-03-16  
; PRIOR APPLICATION NUMBER: 60/052,991  
; PRIOR FILING DATE: 1997-06-11  
; PRIOR APPLICATION NUMBER: 09/095,094  
; PRIOR FILING DATE: 1998-06-10  
; PRIOR APPLICATION NUMBER: 60/126,019  
; PRIOR FILING DATE: 1999-03-24  
; PRIOR APPLICATION NUMBER: 60/134,220  
; PRIOR FILING DATE: 1999-05-14  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 3474  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (247)..(2211)  
; NAME/KEY: sig\_peptide  
; LOCATION: (247)..(366)  
; NAME/KEY: mat\_peptide  
; LOCATION: (367)..(2211)

US-10-041-574-1

Query Match 93.3%; Score 544.8; DB 13; Length 3474;  
Best Local Similarity 97.4%; Pred. No. 1.6e-144;  
Matches 571; Conservative 0; Mismatches 13; Indels 2; Gaps 2;

Qy 1 GCGNCCGCGNNGNCARAGGTGCTTGAGCGCCCTAGNGCCTCCCTTGGCGCTCCCTCC 60  
Db 36 GCGGCGCGCGCGCTGGCAGGTGCTGAGCGCCCTAGAGCCTCCCTTGGCGCTCCCTCC 95  
Qy 61 TCTGCCCGCGCGCTAGCAGTGCACATGCGGTGTTGGAGGTAGATGGGCTCCCGG-CCGGGA 119  
Db 96 TCTGCCCGCGCGCAGCAGTGCACATGCGGTGTTGGAGGTAGATGGGCTCCCGGCGCGGA 155  
Qy 120 GCGGCGGTGATGCGGCGCTGGGCAAGACAGCGCCGATTCAGCTCCCGCGCGCGCC 179  
Db 156 GCGGCGGTGATGCGGCGCTGGGCAAGACAGCGCCGATTCAGCTCCCGCGCGCGCC 215  
Qy 180 CC-GGCACCTTGGAGTCCCGGTTGAGCATGGGGACCTCTCCGAGCAGCAGCAGCCG 238  
Db 216 CCGGGCGCCCTTGGAGTCCCGGTTGAGCATGGGGACCTCTCCGAGCAGCAGCAGCCG 275  
Qy 239 CTTGCGCTCTGAGCGCGCATGCGCGCGGAGCAGCAGCAGCAGCAGCAGCAGCAGC 298  
Db 276 CTTGCGCTCTGAGCGCGCATGCGCGCGGAGCAGCAGCAGCAGCAGCAGCAGCAGC 335  
Qy 299 TCTCTGCTTGGATTCTTACGACCCACACAGCTCAGCCAGAACAGAGGCTTCGAATCT 358  
Db 336 TCTCTGCTTGGATTCTTACGACCCACACAGCTCAGCCAGAACAGAGGCTTCGAATCT 395  
Qy 359 CATTGGCAGATACCGGCATTTGACCGTGCACCGCGCAGGTGTAACCTGTGACAAGTG 418  
Db 396 CATTGGCAGATACCGGCATTTGACCGTGCACCGCGCAGGTGTAACCTGTGACAAGTG 455  
Qy 419 TCCAGCAGGAACCTATGCTCTGAGCATTTGACCATGAGATGGCATAGAGAAATGCCATGCTGTAG 478  
Db 456 TCCAGCAGGAACCTATGCTCTGAGCATTTGACCATGAGATGGCATAGAGAAATGCCATGCTGTAG 515  
Qy 479 TTGCGCTGTGGGACCTTTACAGGCGATGAGATGGCATAGAGAAATGCCATGCTGTAG 538  
Db 516 TTGCGCTGTGGGACCTTTACAGGCGATGAGATGGCATAGAGAAATGCCATGCTGTAG 575  
Qy 539 TCAGCCATGCCCATGCCCAATGATTGAGAAATACCTTTGTGTGCC 584  
Db 576 TCAGCCATGCCCATGCCCAATGATTGAGAAATACCTTTGTGTGCC 621

## RESULT 6

US-10-834-966-1  
; Sequence 1, Application US/10834966  
; Publication No. US20040197870A1  
; GENERAL INFORMATION:  
; APPLICANT: Ni, Jian  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Fan, Ping  
; APPLICANT: Gentz, Reiner L.  
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9  
; FILE REFERENCE: PF375P1  
; CURRENT APPLICATION NUMBER: US/10/834,966  
; CURRENT FILING DATE: 2004-04-30  
; PRIOR APPLICATION NUMBER: US/10/041,574  
; PRIOR FILING DATE: 2002-01-10  
; PRIOR APPLICATION NUMBER: 09/527,236  
; PRIOR FILING DATE: 2000-03-16  
; PRIOR APPLICATION NUMBER: 60/052,991  
; PRIOR FILING DATE: 1997-06-11  
; PRIOR APPLICATION NUMBER: 09/095,094  
; PRIOR FILING DATE: 1998-06-10  
; PRIOR APPLICATION NUMBER: 60/126,019  
; PRIOR FILING DATE: 1999-03-24  
; PRIOR APPLICATION NUMBER: 60/134,220  
; PRIOR FILING DATE: 1999-05-14  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 3474  
; TYPE: DNA  
; ORGANISM: Homo sapiens

FEATURE: ;  
NAME/KEY: CDS ;  
LOCATION: (247) .. (2211) ;  
FEATURE: ;  
NAME/KEY: sig\_peptide ;  
LOCATION: (247) .. (366) ;  
FEATURE: ;  
NAME/KEY: mat\_peptide ;  
LOCATION: (367) .. (2211) ;  
US-10-834-966-1

Query Match 93.38; Score 544.8; DB 18; Length 3474;  
Best Local Similarity 97.44; Pred. No. 1.6e-144;  
Matches 571; Conservative 0; Mismatches 13; Indels 2; Gaps 2;  
QY 1 GCGNCCCGNNGNGCAAGTGCTGAGCGCCCTAGNGCCTCCCTGGCGGCTCCCTCC 60  
DB |||||  
QY 61 TCTGCCCGCGGTAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCG-CCGGGA 119  
DB |||||  
QY 96 TCTGCCCGCGCGAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCGCGCGGA 155  
DB |||||  
QY 120 GCGGGCGGTGATGCGCGCTGGGCAGACAGCGCCGATTCAGTGTCCCGCGGCC 179  
DB |||||  
QY 156 GCGGGCGGTGATGCGCGCTGGGCAGACAGCGCCGATTCAGTGTCCCGCGGCC 215  
DB |||||  
QY 180 CC-GGCCACCTTGGAGTCCCGGTTCCAGCCATGGGGACCTCTCCGAGCAGCAGCCGC 238  
DB |||||  
QY 216 CCGGGCGCCCTGGAGTCCCGGTTCCAGCCATGGGGACCTCTCCGAGCAGCAGCCGC 275  
DB |||||  
QY 239 CTTGCGCTCTGAGCGCGATCGCGCCCGAGCCACAGCCAGTATCGCGGGCTCCCT 298  
DB |||||  
QY 276 CTTGCGCTCTGAGCGCGATCGCGCCCGAGCCACAGCCAGTATCGCGGGCTCCCT 335  
DB |||||  
QY 299 TCTGCTCTTGGATTCTTACGACCCACAGCTCAGCCAGAACAGAGGCTCGAATCT 358  
DB |||||  
QY 336 TCTGCTCTTGGATTCTTACGACCCACAGCTCAGCCAGAACAGAGGCTCGAATCT 395  
DB |||||  
QY 359 CATTTGGCACATACCGCATCTTACCGTCCCGCGCGAGGTCTTACCTGTGCACAGTG 418  
DB |||||  
QY 396 CATTTGGCACATACCGCATCTTACCGTCCCGCGCGAGGTCTTACCTGTGCACAGTG 455  
DB |||||  
QY 419 TCCAGCAGGAACCTATCTCTGAGCATTTGACCAACAGCGCTGCGGCTCTGCAGCAG 478  
DB |||||  
QY 456 TCCAGCAGGAACCTATCTCTGAGCATTTGACCAACAGCGCTGCGGCTCTGCAGCAG 515  
DB |||||  
QY 479 TTGCGCTGTGGGACCTTTACCGGCATGAGATGGCATAGAGAAATGCCATGACTGTAG 538  
DB |||||  
QY 516 TTGCGCTGTGGGACCTTTACCGGCATGAGATGGCATAGAGAAATGCCATGACTGTAG 575  
DB |||||  
QY 539 TCAGCCATGCCATGCCCAATGATTGAGAAATACCTTGCTGCC 584  
DB |||||  
QY 576 TCAGCCATGCCATGCCCAATGATTGAGAAATACCTTGCTGCC 621  
DB |||||

RESULT 7

US-09-978-295A-63  
Sequence 63, Application US/09978295A  
Patent No. US2002015606A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC11  
CURRENT APPLICATION NUMBER: US/09/978,295A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
PRIOR APPLICATION NUMBER: 60/078004  
PRIOR FILING DATE: 1998-03-13  
PRIOR APPLICATION NUMBER: 60/078886  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078936  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078939  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079664  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079663  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079786  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079920  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/079923  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/080105  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080107  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080165

1 PRIOR FILING DATE: 1998-03-31  
2 PRIOR APPLICATION NUMBER: 60/080194  
3 PRIOR FILING DATE: 1998-03-31  
4 PRIOR APPLICATION NUMBER: 60/080327  
5 PRIOR FILING DATE: 1998-04-01  
6 PRIOR APPLICATION NUMBER: 60/080328  
7 PRIOR FILING DATE: 1998-04-01  
8 PRIOR APPLICATION NUMBER: 60/080333  
9 PRIOR FILING DATE: 1998-04-01  
10 PRIOR APPLICATION NUMBER: 60/080334  
11 PRIOR FILING DATE: 1998-04-01  
12 PRIOR APPLICATION NUMBER: 60/081070  
13 PRIOR FILING DATE: 1998-04-08  
14 PRIOR APPLICATION NUMBER: 60/081049  
15 PRIOR FILING DATE: 1998-04-08  
16 PRIOR APPLICATION NUMBER: 60/081071  
17 PRIOR FILING DATE: 1998-04-08  
18 PRIOR APPLICATION NUMBER: 60/081195  
19 PRIOR FILING DATE: 1998-04-08  
20 PRIOR APPLICATION NUMBER: 60/081203  
21 PRIOR FILING DATE: 1998-04-09  
22 PRIOR APPLICATION NUMBER: 60/081229  
23 PRIOR FILING DATE: 1998-04-09  
24 PRIOR APPLICATION NUMBER: 60/081955  
25 PRIOR FILING DATE: 1998-04-15  
26 PRIOR APPLICATION NUMBER: 60/081817  
27 PRIOR FILING DATE: 1998-04-15  
28 PRIOR APPLICATION NUMBER: 60/081819  
29 PRIOR FILING DATE: 1998-04-15  
30 PRIOR APPLICATION NUMBER: 60/081952  
31 PRIOR FILING DATE: 1998-04-15  
32 PRIOR APPLICATION NUMBER: 60/081838  
33 PRIOR FILING DATE: 1998-04-15  
34 PRIOR APPLICATION NUMBER: 60/082568  
35 PRIOR FILING DATE: 1998-04-21  
36 PRIOR APPLICATION NUMBER: 60/082569  
37 PRIOR FILING DATE: 1998-04-21  
38 PRIOR APPLICATION NUMBER: 60/082704  
39 PRIOR FILING DATE: 1998-04-22  
40 PRIOR APPLICATION NUMBER: 60/082804  
41 PRIOR FILING DATE: 1998-04-22  
42 PRIOR APPLICATION NUMBER: 60/082700  
43 PRIOR FILING DATE: 1998-04-22  
44 PRIOR APPLICATION NUMBER: 60/082797  
45 PRIOR FILING DATE: 1998-04-22  
46 PRIOR APPLICATION NUMBER: 60/082796  
47 PRIOR FILING DATE: 1998-04-23  
48 PRIOR APPLICATION NUMBER: 60/083336  
49 PRIOR FILING DATE: 1998-04-27  
50 PRIOR APPLICATION NUMBER: 60/083322  
51 PRIOR FILING DATE: 1998-04-28  
52 PRIOR APPLICATION NUMBER: 60/083392  
53 PRIOR FILING DATE: 1998-04-29  
54 PRIOR APPLICATION NUMBER: 60/083495  
55 PRIOR FILING DATE: 1998-04-29  
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57 PRIOR FILING DATE: 1998-04-29  
58 PRIOR APPLICATION NUMBER: 60/083499  
59 PRIOR FILING DATE: 1998-04-29  
60 PRIOR APPLICATION NUMBER: 60/083545  
61 PRIOR FILING DATE: 1998-04-29  
62 PRIOR APPLICATION NUMBER: 60/083554  
63 PRIOR FILING DATE: 1998-04-29  
64 PRIOR APPLICATION NUMBER: 60/083558  
65 PRIOR FILING DATE: 1998-04-29  
66 PRIOR APPLICATION NUMBER: 60/083559  
67 PRIOR FILING DATE: 1998-04-29  
68 PRIOR APPLICATION NUMBER: 60/083500  
69 PRIOR FILING DATE: 1998-04-29  
70 PRIOR APPLICATION NUMBER: 60/083742  
71 PRIOR FILING DATE: 1998-04-30  
72 PRIOR APPLICATION NUMBER: 60/084366  
73 PRIOR FILING DATE: 1998-05-05

1 PRIOR APPLICATION NUMBER: 60/084414  
2 PRIOR FILING DATE: 1998-05-06  
3 PRIOR APPLICATION NUMBER: 60/084441  
4 PRIOR FILING DATE: 1998-05-06  
5 PRIOR APPLICATION NUMBER: 60/084637  
6 PRIOR FILING DATE: 1998-05-07  
7 PRIOR APPLICATION NUMBER: 60/084639  
8 PRIOR FILING DATE: 1998-05-07  
9 PRIOR APPLICATION NUMBER: 60/084640  
10 PRIOR FILING DATE: 1998-05-07  
11 PRIOR APPLICATION NUMBER: 60/084598  
12 PRIOR FILING DATE: 1998-05-07  
13 PRIOR APPLICATION NUMBER: 60/084600  
14 PRIOR FILING DATE: 1998-05-07  
15 PRIOR APPLICATION NUMBER: 60/084627  
16 PRIOR FILING DATE: 1998-05-07  
17 PRIOR APPLICATION NUMBER: 60/084643  
18 PRIOR FILING DATE: 1998-05-07  
19 PRIOR APPLICATION NUMBER: 60/085339  
20 PRIOR FILING DATE: 1998-05-13  
21 PRIOR APPLICATION NUMBER: 60/085338  
22 PRIOR FILING DATE: 1998-05-13  
23 PRIOR APPLICATION NUMBER: 60/085323  
24 PRIOR FILING DATE: 1998-05-13  
25 PRIOR APPLICATION NUMBER: 60/085582  
26 PRIOR FILING DATE: 1998-05-15  
27 PRIOR APPLICATION NUMBER: 60/085700  
28 PRIOR FILING DATE: 1998-05-15  
29 PRIOR APPLICATION NUMBER: 60/085689  
30 PRIOR FILING DATE: 1998-05-15  
31 PRIOR APPLICATION NUMBER: 60/085579  
32 PRIOR FILING DATE: 1998-05-15  
33 PRIOR APPLICATION NUMBER: 60/085580  
34 PRIOR FILING DATE: 1998-05-15  
35 PRIOR APPLICATION NUMBER: 60/085573  
36 PRIOR FILING DATE: 1998-05-15  
37 PRIOR APPLICATION NUMBER: 60/085704  
38 PRIOR FILING DATE: 1998-05-15  
39 PRIOR APPLICATION NUMBER: 60/085697

Query Match 93.0%; Score 543.2; DB 9; Length 3534;

Best Local Similarity 97.3%; Pred. No. 4.4e-144;

Matches 570; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

QY 1 GCGNCGGNGNGNGCAAGGTGCTGAGCGCCCTAGNCCCTCCCTGCGGCTCCCTCC 60  
Db 114 GCGGCTCGCGCTCGCGCTGAGCGCCCTAGAGCTCCCTTGCCTCCCTCCCTCC 173  
QY 61 TCTGCCCGCGCTAGCAGTGACATGGGGTGTGGAGGTAGATGGGCTCCCGG-CCGGGA 119  
Db 174 TCTGCCCGCGCTAGCAGTGACATGGGGTGTGGAGGTAGATGGGCTCCCGGCGGGA 233  
QY 120 GCGCGGCTGGATGCGGCGCTGGGAGAGCAGCGCGGATTCAGCTGCTCCCGGCGGC 179  
Db 234 GCGCGGCTGGATGCGGCGCTGGGAGAGCAGCGCGGATTCAGCTGCTCCCGGCGGC 293  
QY 180 CC-GGCCACCTTGCAGTCCCGGTTAGCCATGGGGACCTCCCGAGCAGCAGCAGCCG 238  
Db 294 CCGGGCGCCCTGCGAGTCCCGGTTAGCCATGGGGACCTCCCGAGCAGCAGCAGCCG 353  
QY 239 CCGCGCTCCTGACGCGCATCGCGCGGAGCAGCAGCAGATGATCGCGGGTCCCT 298  
Db 354 CCGCGCTCCTGACGCGCATCGCGCGGAGCAGCAGCAGATGATCGCGGGTCCCT 413  
QY 299 TCTCTGCTGGATTCCCTTAGCACCACCAAGCTCAGCAGCAGCAGCAGCAGCTCGAATCT 358  
Db 414 TCTCTGCTGGATTCCCTTAGCACCACCAAGCTCAGCAGCAGCAGCAGCAGCTCGAATCT 473  
QY 359 CATTCGCACATACCGCCATGTTGACGCTGCCCGCCAGGTGCTAACTGTGACAAGTG 418  
Db 474 CATTCGCACATACCGCCATGTTGACGCTGCCCGCCAGGTGCTAACTGTGACAAGTG 533  
QY 419 TCCAGCAGGAACCTATGTCTCTGAGCATTTGTACCAACAAGCCTGCGGCTGTGACGAG 478

Db 534 TCCAGCAGGAACTATGCTCTGAGCAATTGTACCAACACAAGCCTGCGCTCTGCAGCAG 593  
Qy 479 TTGCCCTGTGGGGACCTTTTACCAGGCATGAGAAATGGCATAGAGAAATGCCATGACTGTAG 538  
Db 594 TTGCCCTGTGGGGACCTTTTACCAGGCATGAGAAATGGCATAGAGAAATGCCATGACTGTAG 653  
Qy 539 TCAGCCATGCCCATGGCCAAATGATTGAGAAATACCTTTGTGCTGCC 584  
Db 654 TCAGCCATGCCCATGGCCAAATGATTGAGAAATACCTTTGTGCTGCC 699

RESULT 8  
US-09-978-697-63  
; Sequence 63, Application US/09978697  
; Patent No. US20020169284A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Flivaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
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; GENERAL INFORMATION:  
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; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
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;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
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; PRIOR APPLICATION NUMBER: 60/085700  
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; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085704  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 93.0%; Score 543.2; DB 9; Length 3534;

Best Local Similarity 97.3%; Pred. No. 4.4e-144;

Matches 570; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

QY 1 GCGNCCGCGNNGNCAAGGTGCTGAGCGCCCTAGNGCCTCCCTTGGCGCTCCCTCC 60

Db 114 GCGGCTCGCGCGCTGGGCGAGTGTGAGCGCCCTAGAGCTCCCTTGGCGCTCCCTCC 173

QY 61 TCTGCCGCGCGCTAGCAGTGCACATGGGTGTTGGAGGTAGATGGCTCCCGG-CCGGGA 119

Db 174 TCTGCCGCGCGCGCAGCAGTGCACATGGGTGTTGGAGGTAGATGGGTCCCGCGCCGGGA 233

QY 120 GCGGCGGTGGATGCGCGCTGGGCGAGAGCAGCCCGGATTCAGTGTGCCCGCGGCC 179

Db 234 GCGGCGGTGGATGCGCGCTGGGCGAGAGCAGCCCGGATTCAGTGTGCCCGCGGCC 293

QY 180 CC-GGCCACCTTCGAGTCCCGGTTTCAGCCATGGGGACCTTCGAGCAGCAGCACCGC 238

Db 294 CCGGCGCGCCCTTCGAGTCCCGGTTTCAGCCATGGGGACCTTCGAGCAGCAGCACCGC 353



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; PRIOR FILING DATE: 1998-05-15  
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; PRIOR APPLICATION NUMBER: 60/085704  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697  
  
Query Match 93.0%; Score 543.2; DB 10; Length 3534;  
Best Local Similarity 97.3%; Pred. No. 4.4e-144;  
Matches 570; Conservative 0; Mismatches 14; Indels 2; Gaps 2;  
  
QY 1 GCGNCGCGNNGNGCAAGTGCTGAGCGCCCTAGNGCCTCCCTTGGCGCCTCCCTCC 60  
DB 114 GCGGCTTCGCGCTGGGAGGTGCTGAGCGCCCTAGAGCCTCCCTTGGCGCCTCCCTCC 173  
QY 61 TCTGCGCGCGCTGAGTGACATGGGGTGTGGAGGTAGATGGGCTCCCGG-CCGGGA 119  
DB 174 TCTGCGCGCGCGAGTGACATGGGGTGTGGAGGTAGATGGGCTCCCGGCGGGGA 233  
QY 120 GCGGCGGTGGATGCGCGCTGGGAGAGAGCAGCGCGGATTCACGTGCGCGCGGCC 179  
DB 234 GCGGCGGTGGATGCGCGCTGGGAGAGAGCAGCGCGGATTCACGTGCGCGCGGCC 293  
QY 180 CC-GGCGACCTTCGCGAGTCCCGGTTTCAGCCATGGGGACCTCTCCGAGCAGCAGCACCGC 238  
DB 294 CCGGCGCGCGCTGCGAGTCCCGGTTTCAGCCATGGGGACCTCTCCGAGCAGCAGCACCGC 353  
QY 239 CTTGCGCTCTGCGAGCGCGATGCGCGCGAGCCACAGCCACGATGATCGCGGGCTCCCT 298  
DB 354 CTTGCGCTCTGCGAGCGCGATGCGCGCGAGCCACAGCCACGATGATCGCGGGCTCCCT 413  
QY 299 TCTCTGCTTGGATTCTTAGCACACCGAGCTGAGCCAGCCAGCCAGCCAGCCAGCCAGCC 358  
DB 414 TCTCTGCTTGGATTCTTAGCACACCGAGCTGAGCCAGCCAGCCAGCCAGCCAGCCAGCC 473  
QY 359 CATTTGCACATACCGCATGTTGACCGTGCCACCGCGCCAGGTCTTAACCTGTGACAAAGTG 418  
DB 474 CATTTGCACATACCGCATGTTGACCGTGCCACCGCGCCAGGTCTTAACCTGTGACAAAGTG 533  
QY 419 TCCAGCAGGAACCTATGTCTCTGAGCATTGTACCAACACAAAGCCTGCGGCTTGCAGCAG 478  
DB 534 TCCAGCAGGAACCTATGTCTCTGAGCATTGTACCAACACAAAGCCTGCGGCTTGCAGCAG 593  
QY 479 TTGCGCTGTGGGACCTTTTACAGGATGAGAAATGAGAAATGCCATGACTGTAG 538  
DB 594 TTGCGCTGTGGGACCTTTTACAGGATGAGAAATGAGAAATGCCATGACTGTAG 653  
QY 539 TCAGCCATGCCCATGCCCAATGATTGAGAAATTTACCTTTGTGTGCC 584  
DB 654 TCAGCCATGCCCATGCCCAATGATTGAGAAATTTACCTTTGTGTGCC 699

RESULT 12  
US-09-978-608A-63  
; Sequence 63, Application US/09978608A  
; Publication No. US20030045462A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Baton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.

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/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Kljavin, Ivar J.
/ APPLICANT: Kuo, Sophia S.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James;
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Shelton, David L.
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE REFERENCE: P2630PIC22
/ CURRENT APPLICATION NUMBER: US/09/978,608A
/ CURRENT FILING DATE: 2001-10-16
/ NUMBER OF SEQ ID NOS: 624
/ Prior Application removed - See File Wrapper or Palm
/ SEQ ID NO 63
/ LENGTH: 3534
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-978-608A-63

Query Match          93.0%; Score 543.2; DB 10; Length 3534;
Best Local Similarity 97.3%; Pred. No. 4.4e-144;
Matches 570; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

QY 1 GCGGCCGCGNNGNGCAAGTGTCTGAGCGCCCTAGNGCCTCCCTTGGCGCTCCCTCC 60
Db 114 GCGGCTCGCGCTGGCAGTGTCTGAGCGCCCTAGAGCTCCCTTGGCGCTCCCTCC 173
QY 61 TCTGCCCGCGCTAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCGG 119
Db 174 TCTGCCCGCGCGCAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCGCGGGA 233
QY 120 GCGCGGGTGTGGTGGCGGCTGGGAGAGCAGCGCCGATTCAGCTGCGCGCGCC 179
Db 234 GCGCGGGTGTGGTGGCGGCTGGGAGAGCAGCGCCGATTCAGCTGCGCGCGCC 293
QY 180 CC-GGCGACCTTCGAGTCCCGGTTCCAGCATGGGGACCTCCGAGCAGCAGCACCGC 238
Db 294 CCGGGCGCCCTCGAGTCCCGGTTCCAGCATGGGGACCTCCGAGCAGCAGCACCGC 353
QY 239 CTTGGCTCTCTGAGCGCATGCGCGCGAGCCAGCCACGATGATCGCGGCTCCCT 298
Db 354 CTTGGCTCTCTGAGCGCATGCGCGCGAGCCAGCCACGATGATCGCGGCTCCCT 413
QY 299 TCTCTGCTTGGATTCTTAGCACCACAGCTGAGCGGAGTCTTACCTGTGCAAGTG 358
Db 414 TCTCTGCTTGGATTCTTAGCACCACAGCTGAGCGGAGTCTTACCTGTGCAAGTG 473
QY 359 CATTGGCACATACCGCATGTTGACCGTGCCACCGCGAGTCTTACCTGTGCAAGTG 418
Db 474 CATTGGCACATACCGCATGTTGACCGTGCCACCGCGAGTCTTACCTGTGCAAGTG 533
QY 419 TCAGCAGGAACCTATGTCTCTGAGATTGTACCAACAGAGCTCGGCTGTGAGCAG 478
Db 534 TCAGCAGGAACCTATGTCTCTGAGATTGTACCAACAGAGCTCGGCTGTGAGCAG 593
QY 479 TTGCGCTGTGGGACCTTTACAGGATGAGATGGCATAGAGAAATGCCATGCTGTAG 538
Db 594 TTGCGCTGTGGGACCTTTACAGGATGAGATGGCATAGAGAAATGCCATGCTGTAG 653
QY 539 TCAGCATGCCATGCCATGATTCAGAAATTAACCTTTGCTGCC 584
Db 654 TCAGCATGCCATGCCATGATTCAGAAATTAACCTTTGCTGCC 699
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/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Baker Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan
/ APPLICANT: Ferrara, Napoleon
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gottard, Audrey
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Kljavin, Ivar J.
/ APPLICANT: Kuo, Sophia S.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James;
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Shelton, David L.
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE REFERENCE: P2630PIC15
/ CURRENT APPLICATION NUMBER: US/09/978,585A
/ CURRENT FILING DATE: 2001-10-16
/ NUMBER OF SEQ ID NOS: 624
/ Prior Application removed - See File Wrapper or Palm
/ SEQ ID NO 53
/ LENGTH: 3534
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-978-585A-63
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Query Match          93.0%; Score 543.2; DB 10; Length 3534;
Best Local Similarity 97.3%; Pred. No. 4.4e-144;
Matches 570; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

QY 1 GCGGCCGCGNNGNGCAAGTGTCTGAGCGCCCTAGNGCCTCCCTTGGCGCTCCCTCC 60
Db 114 GCGGCTCGCGCTGGCAGTGTCTGAGCGCCCTAGAGCTCCCTTGGCGCTCCCTCC 173
QY 61 TCTGCCCGCGCTAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCGG 119
Db 174 TCTGCCCGCGCGCAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCGCGGGA 233
QY 120 GCGCGGGTGTGGTGGCGGCTGGGAGAGCAGCGCCGATTCAGCTGCGCGCGCC 179
Db 234 GCGCGGGTGTGGTGGCGGCTGGGAGAGCAGCGCCGATTCAGCTGCGCGCGCC 293
QY 180 CC-GGCGACCTTCGAGTCCCGGTTCCAGCATGGGGACCTCCGAGCAGCAGCACCGC 238
Db 294 CCGGGCGCCCTCGAGTCCCGGTTCCAGCATGGGGACCTCCGAGCAGCAGCACCGC 353
QY 239 CTTGGCTCTCTGAGCGCATGCGCGCGAGCCAGCCACGATGATCGCGGCTCCCT 298
Db 354 CTTGGCTCTCTGAGCGCATGCGCGCGAGCCAGCCACGATGATCGCGGCTCCCT 413
QY 299 TCTCTGCTTGGATTCTTAGCACCACAGCTGAGCGGAGTCTTACCTGTGCAAGTG 358
Db 414 TCTCTGCTTGGATTCTTAGCACCACAGCTGAGCGGAGTCTTACCTGTGCAAGTG 473
QY 359 CATTGGCACATACCGCATGTTGACCGTGCCACCGCGAGTCTTACCTGTGCAAGTG 418
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Db 474 CATTGGCACATACCGCCATGTGACCGTGCCACCGCCAGGTGTACCTGTGACAGTG 533  
Qy 419 TCAGCAGGAACCTATGCTCTGAGCATTTGACCAACAAAGCTGGCGTCTGACGACG 478  
Db 534 TCAGCAGGAACCTATGCTCTGAGCATTTGACCAACAAAGCTGGCGTCTGACGACG 593  
Qy 479 TTGCCCTGTGGGACCTTTTACCAAGGCATGAGAAATGCCATGACCTGTAG 538  
Db 594 TTGCCCTGTGGGACCTTTTACCAAGGCATGAGAAATGCCATGACCTGTAG 653  
Qy 539 TCAGCCATGCCCATGGCCATGATTGAGAAATACCTTTGCTGCC 584  
Db 654 TCAGCCATGCCCATGGCCATGATTGAGAAATACCTTTGCTGCC 699

## RESULT 14

US-09-978-191A-63

; Sequence 63, Application US/09978191A

; Publication No. US20030050239A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnovers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin U.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kijavlin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2630P1C4

; CURRENT APPLICATION NUMBER: US/09/978,191A

; PRIOR FILING DATE: 2001-10-15

; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/064249

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;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085700  
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;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085579  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085580  
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;; PRIOR APPLICATION NUMBER: 60/085573  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085704  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 93.0%; Score 543.2; DB 10; Length 3534;  
Best Local Similarity 97.3%; Pred. No. 4.4e-144;  
Matches 570; Conservative 0; Mismatches 14; Indels 2; Gaps 2;  
  
QY 1 GCGNCCGGNNGNGCAAGTGTGAGCGCCCTAGNCGCTTCCCTTGGCGCTCCCTCC 60  
DB 114 GGGGCTCGCGCTGGCGAGGTGCTGAGCGCCCTAGAGCCCTCCCTTGGCGCTCCCTCC 173  
  
QY 61 TCTGCGCGCGCTAGCAGTGCATGGGGTGTGAGGTAGATGGCTCCCGG-CGGGA 119  
DB 174 TCTGCGCGCGCGCAGCAGTGCATGGGGTGTGAGGTAGATGGCTCCCGCGCGGA 233  
  
QY 120 GCGCGGGTGGATGCGGGCTGGGCGAGAGCAGCGCCGATTCCAGCTGCCCCGGCGCC 179  
DB 234 GCGCGGGTGGATGCGGGCTGGGCGAGAGCAGCGCCGATTCCAGCTGCCCCGGCGCC 293  
  
QY 180 CC-GGCCACCTTGGCGAGTCCCCGGTTACGCCATGGGGACCTCTCCGAGCAGCAGCCGC 238  
DB 294 CCGGGCGCCCTGCGAGTCCCCGGTTACGCCATGGGGACCTCTCCGAGCAGCAGCCGC 353  
  
QY 239 CTTGCGCTCTGCGAGCGCGCATGCGCGCGGAGCCACAGCCAGTATCGCGGCTCCCT 298  
DB 354 CTTGCGCTCTGCGAGCGCGCATGCGCGCGGAGCCACAGCCAGTATCGCGGCTCCCT 413  
  
QY 299 TCTCTGCTTGGATTCTTAGCACCACACAGCTCAGCCAGAACAGAGGCTCGAATCT 358  
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QY 359 CATGGCACATACCGCCATGTTGACCGTGCACACCGCCAGGTGCTAACTGTGACAAGTG 418  
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QY 419 TCCAGCAGGACCTATGCTCTGAGCATTGTACCAACCAAGCCCTGCGGTCTGCAGCAG 478  
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QY 479 TTGCGCTGTGGGACCTTTACCAGGCATGAGAATGGCATAGAGAATGCCATGACTGTAG 538  
DB 594 TTGCGCTGTGGGACCTTTACCAGGCATGAGAATGGCATAGAGAATGCCATGACTGTAG 653  
  
QY 539 TCAGCCATGCCCATGGCCAAATGATTGAGAAATTAATCTTGTGTGCTGCC 584  
DB 654 TCAGCCATGCCCATGGCCAAATGATTGAGAAATTAATCTTGTGTGCTGCC 699  
  
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; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630P1C17  
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CURRENT FILING DATE: 2002-03-19  
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| Query Match           | 93.0%;          | Score 543.2;   | DB 10;    | Length 3534; |
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| Best Local Similarity | 97.3%;          | Pred. No. 4.4e-144;  |           |              |
| Matches 570;          | Conservative 0; | Mismatches 14;   | Indels 2; | Gaps 2;      |
| QY                    | 1               | GCNCGCCGNGNGNCAGAGTGCTGAGCGCCCTAGNGCCTCCCTTCGCGCCTCCCTCC     | 60        |              |
| Db                    | 114             | GCGCCCTCGCGCTGGCGAGGTGCTGAGCGCCCTTAGAGCCTCCCTTCGCGCCTCCCTCC  | 173       |              |
| QY                    | 61              | TCTGCCCGCGCTAGCAGTCACATGGGTGTTGGAGGTAGATGGCTCCCGG-CCGGGA     | 119       |              |
| Db                    | 174             | TCTGCCCGCGCAGCAGTCACATGGGTGTTGGAGGTAGATGGCTCCCGGCCGGGA       | 233       |              |
| QY                    | 120             | GGCGGGGTGGATGCGGGCTGGGCAGAGCAGCGCCCGATTCACGTGCCCGCGGCGCC     | 179       |              |
| Db                    | 234             | GGCGGGGTGGATGCGGGCTGGGCAGAGCAGCGCGCGATTCACGTGCCCGCGGCGCC     | 293       |              |
| QY                    | 180             | CC-GGCCACCTTGGAGTCCCGGTTTCAGCCATGGGACCTCTCCGAGCAGCAGCACGCG   | 238       |              |
| Db                    | 294             | CCGGCGCCCTTCGAGTCCCGGTTTCAGCCATGGGACCTCTCCGAGCAGCAGCACGCG    | 353       |              |
| QY                    | 239             | CCTCGCCTCTGCAGCGCGCATTCGCCCGCGAGCCACAGCCACGATGATCGCGGGTCCT   | 298       |              |
| Db                    | 354             | CCTCGCCTCTGCAGCGCGCATTCGCCCGCGAGCCACAGCCACGATGATCGCGGGTCCT   | 413       |              |
| QY                    | 299             | TCTCTGCTTGGATTCTCTTAGCACCCACACAGCTCAGCCAGAACAGAGGGCTCGAATCT  | 358       |              |
| Db                    | 414             | TCTCTGCTTGGATTCTCTTAGCACCCACAGCTCAGCCAGAACAGAGGGCTCGAATCT    | 473       |              |
| QY                    | 359             | CATTGGCACATACGCCCATGTTGACCGTGCCACCGGCCAGGTGCTAACTGTGACAAGT   | 418       |              |
| Db                    | 474             | CATTGGCACATACGCCCATGTTGACCGTGCCACCGGCCAGGTGCTAACTGTGACAAGT   | 533       |              |
| QY                    | 419             | TCAGCAGGAACTATGCTCTGAGCATTGTACCAACACAGCCTGCGCGTCTGCAGAG      | 478       |              |
| Db                    | 534             | TCAGCAGGAACTATGCTCTGAGCATTGTACCAACACAGCCTGCGCGTCTGCAGAG      | 593       |              |
| QY                    | 479             | TTGCCCTGTGGGACCTTTTACAGGCATGAGAAATGGCATAGAGAAATGCCATGACTGTAG | 538       |              |
| Db                    | 594             | TTGCCCTGTGGGACCTTTTACAGGCATGAGAAATGGCATAGAGAAATGCCATGACTGTAG | 653       |              |
| QY                    | 539             | TCAGCCATGCCCATGGCCATGATTAGAAATACCTTGTGCTGCC                  | 584       |              |
| Db                    | 654             | TCAGCCATGCCCATGGCCATGATTAGAAATACCTTGTGCTGCC                  | 699       |              |